

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 144864

TO: Jeffrey Parkin

Location: rem/3d39/3c18

Art Unit: 1648

Monday, February 28, 2005

Case Serial Number: 09/319156

From: Deirdre Arnold

Location: Biotech-Chem Library

REM 1A64

Phone: 571-272-2532

Deirdre.Arnold@uspto.gov

Search Notes

Please contact me if you encounter any problems with the disk or files.

Note that results are not generally sent via e-mail because the files are often very large.

Please feel free to contact me if you have any questions or would like to amend the search.

Thank you for using STIC services.

Regards, Deirdre Arnold



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STIC-Biotech/ChemLib

From:

Parkin, Jeffrey

Sent:

Wednesday, February 09, 2005 9:52 PM

To: Subject: STIC-Biotech/ChemLib

U.S. Serial No. 09/319,156

Please search SEQ ID NOS.: 6, 9, and 12 from the aforementioned application v. all relevant databases, including interference.

Type of Search

NA Sequence: #_

AA Sequence:#

Place results on both PAPER and electronic format (i.e., e-mail).

Provide the first 40 results for each search.

Thanks!

JSP AU 1648 REM 3D39 2-0908

http://expoweb1:8001/cgi-bin/expo/GenInfo/snguery.pl?APPL_ID=09319156

STAFF USE ONLY

Searcher: Anolog Searcher Phone: 2-2 Date Searcher Picked up Date Completed: Searcher Prep/Rev. Time:

Structure: #_ Bibliographic: Litigation: Patent Family: Online Time:_ Other:_

Vendors and cost where applicable STN:_ DIALOG: QUESTEL/ORBIT: LEXIS/NEXIS: SEQUENCE SYSTEM Com www/Internet:

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Ott.C. and Bedin,F.
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PATENT: WO 9902666-A 6 21-JAN-1999;
BIO MERIEUX (FR); OTT CATHERINE (FR)
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Perron, H., Beseme, F., Bedin, F., Paranhos-Baccala, G., Komurian-Pradel, F., Jolivet-Reynaud, C. and Mandrand, B. Isolated nucleotide sequences associated with multiple rheumatoid arthritis and a process of detecting Parent: Use 582703-A 102 24-UNN-2003;

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                 /organism="unidentified"
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                                                                                            CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAACTGTAAAACTA
                                                                                                                                                             CIGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
                                                                                                                                                                        CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC
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                                                                                                                                                                                                      GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGGAAGCAGTTAGAGCGGT
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                                                                                CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCCTTCCAGAATCAAAACTGTAAAACTA
                                                             Gaps
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Viruses; Retroid viruses; Retrovirus element
Viruses; Retroid viruses; Retroviridae.

1 (bases 1 to 2004)

2 Komurian-Pradel,F., Paranhos-Baccala,G., Bedin,F.,
Vunanian-Paraz,A., Sodoyer,M., Ott,C., Rajoharison,A., Gark
Mallet,F., Mandrand,B. and Perron,H.
Molecular cloning and characterization of MSRV-related sequasociated with retrovirus-like particles

1 Virology 260 (1), 1-9 (1999)

1 10405350
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                                         Length 635;
                                                            Indela
                                         Score 635; DB 6; L
Pred. No. 1.1e-189;
; Mismatches 0;
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  /mol_type="unassigned I
/db_xref="taxon:32644"
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                                         100.0%;
llarity 100.0%;
Conservative 0
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                                                   Similarity
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Best Local Simi
Matches 635;
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                                         Garcia, E.,
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2 (bases 1 to 2004)
Komurian-Pradel, F., Paranhos-Baccala, G., Bedin, F.,
Komurian-Pradel, F., Sodoyer, M., Ott, C., Rajoharison, A., (
Mallet, F., Mandrand, B. and Perron, H.

Direct Submission
Submitted (10-FBB-1999) UMR103 CNRS, bioMerieux, 46, al)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               Length 2004;
                                                                                                                                                                                          /organism="Multiple sclerosis associated element"
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                                                                                                                                                                                                                                                                                                 1. .2004
/note="gimilar to pol-env and 3'LTR
                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 635; DB 14;
100.0%; Pred. No. 1.3e-189;
ive 0; Mismatches 0;
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KEYWORDS

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McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Muenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retterson, K., Ribedok, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retter, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travers, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

AL Submitted (25-APR-2002) Whitehead Institute/MIT Center for Genome Research 320 Charles Street, Cambridge, MA 02141, USA On Mar 22, 2002 this sequence version replaced gill887526.

All repeats were identified using RepeatMasker: html

Lender: Whitehead Institute/ MIT Center for Genome Research Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_Information
Center project name: L24497
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complement(12442. .13393)
/rpt_family="L1PA16"
13550. .13907
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/rpt family="LiM4"
complement (8444. .8971)
/rpt family="LiME3A"
complement (8973. .9386)
/rpt family="LiME3A"
complement (9387. .9690)
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1898. .10497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="MIR"
6723. .6750
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6982. .7280
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/rpt_family="AT_rich"
3108. 3127
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/rpt family="(TA)n"

3128...3128

1154...3208

/rpt family="(TG)n"

/rpt family="(TA)n"

complement (3212...381)

/rpt family="LIMA9"
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5234. .6028
/rpt_family="L1ME3"
complement (6259. .647
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Andereon, S., Barna, N., Bartieria, V., Bogularakty, L., Boubhagaler, B., Andereon, S., Barna, N., Bartieria, V., Bogularakty, J., Colangola, C., Campopiano, A., Chang, J., Chazaro, B., Choopel, Y., Colangelo, M., Collimo, S., Collimore, A., Cook, D., Cocke, P., Daratas, M., Especial, M., Canda, J., Choopel, S., Cookel, D., Colangelo, M., Collimo, S., Collimo, S., Cookel, P., Daratas, M., Sakaras, M., Caraba, J., Colangelo, M., Collimo, S., Cookel, P., Daratas, M., Sakaras, M., Caraba, M., Carada, P., Carada, P., Carada, P., Carada, M., Carada, 
                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I bases I to 167594)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo. sapiens chromosome 18; clone RP11-62209
                                                                                                                                                                                                                                                             (bases 1 to 167694)
                                                                                                                                                                                                                                   Unpublished
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List (absent Lordy).

Sitzen, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Colespel, Y., Colangelo, M., Bown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Handand, J.C., Johnson, R., Jevine, R., Lieu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Maddonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Sancos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

Direct Submission

No noct 25, 2001 this sequence version replaced gi:7230183.

All repeats were identified using RepeatMasker:

Smit, A. F. A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                         123190
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123369 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC 123310
                                                                 123250
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Homo sapiens chromosome 18 clone RP11-497M7 map 18, WORKING DRAFT
SEQUENCE.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 176095)
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                                                                                                                        ACTAMANTGCTMATTAGGCMAMATAGGAGGTMANGAMATAGCCMATCATCTATTGCCTG
                                                                                                                                                                                                                                         481 AGAGCACAGCGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
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AC019346.4 GI:16418201
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
HOMO sapiens (human)
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KEYWORDS
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Pred. No. 2.9e-188;
0; Mismatches 2;
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'note="<30 qual SNGL region"

complement (26144. .26248)

'rpt family="MIR"

1732. .27794
                                                                                                                                                                                                                                                                  /rpt_family="L1MB3"
complement(20633. .22006)
/rpt_family="L1P"
22008. .22831
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complement(32304. .34133)
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/rpt_family="AT_rich"
24886. .24913
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/rpt family="GA-rich"
complement (30946. .310
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rpt_family="(TAGA)n"
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                                                                                                                                                                                    , oc4. .18430
/rpt_family="L1PA4"
18441. .1900
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22853. 23516
/rpt_family="L2"
24420. 24468
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family="MER67C"
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17572. 17628
/rpt_family="LiM4"
/rpt_family="LiM4"
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8013. .28078
                                 'rpt_family="L1PB1"
5633. .15912
                                                                            rpt family="(TA)n"
5920. .16279
                                                                                                             family="L1PB1"
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9293. .20623
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Best Local Similarity 99.7
Matches 633; Conservative
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1 (bases 1 to 210336)
Abola, A.P., Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D., Federspiel, N., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R., Mano, J., Komp, C., Kottler, S., Lam, B., Marathe, R., Miranda, M., Morehouse, A.J., Nguyen, M., Oefner, P., Palm, C.J., Ramirez, D., Southwick, A.M., Webb, C., Wilhelmy, J., Yu, S. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (26-JAN-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .------ Genome Center
Center: Stanford DNA Sequencing and Technology Development
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Bruno,D., Conn,L., Dela Rosa,M., Federspiel,N., Foreman,P.,
Glukhov,S., Hansen,N., Hyman,R., Mao,J., Marathe,R.,
Morehouse,A.J., Oefner,P., Palm,C.J., Ramirez,D., Wilhelmy,J.,
Yu,S. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing Vector: plasmid; R02513; 97% of reads Sequencing Vector: plasmid; plasmid_accession; 3% of read Chemistry: Dye-primer; 10% of reads Chemistry: Dye-terminator Big Dye; 88% of reads Chemistry: Dye-terminator Big Dye; 88% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 208312 bases at least Q40 Consensus quality: 20837 bases at least Q20 Consensus quality: 209157 bases at least Q20 Insert size: 199762; agarcose-fp Insert size: 199762; agarcose-fp Insert size: 210236; sun-of-contigs Quality coverage: 8.7x in Q20 bases; agarcos-fp Quality coverage: 8.7x in Q20 bases; sum-of-contigs.

* NOTE: This is a "working draft' sequence: It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://sequence-www.stanford.edu/group/human/
Contact: hum-info@sequence.stanford.edu
------- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                    ACO22171
Homo sapiens chromosome 18 clone RP11-407C18, WORKING DRAFT
SCOURNCE, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC022171.18 GI:13270574
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Mar 10, 2001 this sequence version replaced gi:13122770.
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Center clone name: RP11-407C18
------ Summary Statistics
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Center project Information

Center project name: 14296

Center clone name: 2420 M J

Sequencing vector: M3; M7815; 32% of reads
Sequencing vector: M3; M7815; 32% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 176095 bases at least Q40

Consensus quality: 176095 bases at least Q30

Insert size: 176095; sum-of-contigs

Quality coverage: 11.5 in Q20 bases; agarose-fp

Quality coverage: 11.7 in Q20

* NOTE: This is a 'working draft' sequence. It currently
consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces
of the gaps between them are based on estimates that have
provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* I 176095; contig of 176095 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150464 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="RP11-497M7"
/clone_lib="RPCI-11 Human Male BAC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic_DN
/db_xref="taxon:9606"
/chromosome="18"
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Submitted (2-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON MAX 30, 2000 this sequence version replaced gi:6087973. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.wahington.edu/RM/RepeatMasker.html
                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 148724)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert size: 182000; agarose-fp
Insert size: 148024; sum-of-contigg
Quality coverage: 3.9 in Q20 bases; agarose-fp
Quality coverage: 4.8 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0: contig of 752 bp in length
0: gap of 100 bp
9: contig of 9159 bp in length
9: ag of 100 bp
5: contig of 16747 bp in length
5: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2462: contig of 2462 bp in length
2562: gap of 100 bp
7948: contig of 5386 bp in length
8048: gap of 100 bp
                                                                                                               Birren, B., Lincon, L., Nusbaum, C. and Lander, B. Homo sapiens, clone RP11-2N15
Unpublished
                HTG; HTGS PHASE1; HTGS DRAFT.
Homo sapiens (human)
 GI:7341824
                                                                                                                                                                      (bases 1 to 148724)
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25059:
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41906:
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63342
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              KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58176 cccretarcritaaccrccricrraagririgicricriccagaarcaaaaccgraaaacra
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACGTGGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGACTGAGAGAC
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                                                                                                                                                                                                                                                                                                                                                                                  1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAACTGTAAAACTA
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 9 66568: gap of unknown length9 210336: contig of 143768 bp in length.Location/Qualifiers
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                                                                                                                                                        clone_lib="RPCI human BAC library 11"
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                                                                                                                                                                                                                                                                                                                Score 631.8; DB 2;
Pred. No. 3e-188;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  601 ATTAAATCTTGCAACTGAAAAAAAAAAAAAAA 635
                                                                                                                                                                      1. .66468
/note="assembly_name:Contig44
                                                                                                                                                                                                                                              /note="assembly_name:Contig45
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                                                                     /organism="Homo sapiens"
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/mol_type="genomic DNA"
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/chromosome="18"
/clone="RP11-407C18"
                                                                                                                                                                                                            clone_end:T7" 665697 .210336
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.7%;
Matches 633; Conservative
                                                         1, .210336
                                                                                                                                                                                                                              misc_feature
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AC010778/c
LOCUS
                                         FEATURES
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contig of 21335 bp in length gap of 100 bp contig of 35146 bp in length

63341: 98587:

AC010778 148724 bp DNA linear HTG 30-MAR-2000 Homo sapiens clone RP11-2N15, WORKING DRAFT SEQUENCE, 8 unordered

pieces. AC010778

DEFINITION ACCESSION

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Direct Submission

Direct Submission

Submitted (12-Nov-2011) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

buring sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

The following abbreviations are used to associate primary accession

numbers given in the feature table with their source databases:

Em; EMBL; Sw.; SMISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information

on the WORNEPE database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence

was generated from part of bacterial clone contigs of human

chromosome X, constructed by the Sanger Centre Chromosome X Mapping

Group. Further information can be found at

http://www.aanger.ac.uk/HGP/ChxX

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (1.e., phred quality >=

10); an attempt was made to resolve all sequencing problems, such

assembly was confirmed by restriction digest. RP6-198C4 is from the

library RRCI-c constructed by the group of Pieter de Jong. For

further details see

http://www.chori.org/bacpac/home.htm

WBCTOR: PROCE.
                                                                                                                                      AL162912

Human DNA sequence from clone RP6-198C4 on chromosome Xq13.3-21.2, complete sequence.
AL165912 AL121824
AL162912.1 GI:7406722
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5635. .5673
/note="HERV17 repeat: matches 7419. .7457 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5956. :6136
/note="LTR17 repeat: matches 1. .239 of consensus"
6195. :6280
/note="LTR17 repeat: matches 239. .324 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMPORTANT: This sequence is not the entire insert of clone RP6-198C4 It may be shorter because we sequence overlapping sections only once, except for a short overlap. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    664. .5955
hote="HERV17 repeat: matches 8244. .8523 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .5930 of
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note="HERV17 repeat: matches 368.
                        601 ATTAAATCTTGCAACTGAAAAAAAAAAAAAA 633
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_lib="RPCI-6"
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/map="q13.3-21.2"
/clone="RP6-198C4"
                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 8339)
                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                            Pearce, A.
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AUTHORS
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AL162912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG 180
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18 98687: gap of 100 bp
18 148724: contig of 50037 bp in length.
Location/Qualifiers
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                                                CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA
                         Gaps
                        ;
Length 8339;
                        Indels
Score 579.2; DB 9;
Pred. No. 8.4e-172;
0; Mismatches 33;
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 Query Match
Best Local Similarity 94.8%;
Matches 599; Conservative
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Homo sapiens (human) DEFINITION ACCESSION VERSION KEYWORDS SOURCE RESULT 10 AC073626/c ORGANISM

PRI 30-JAN-2004 linear PRI 30-complete sequence. ACU73626 136901 bp DNA Homo sapiens BAC clone RP11-95P9 from 7, AC073626

AC073626.7 GI:12863221

REFERENCE AUTHORS

Districts, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E. (bases 1 to 1360µ).

E. (bases 1 to 1360µ).

Hillier L.W., Fulton, R.S., Fulton, L.A., Graves, T.A., Pepin, K.H., Magner-McPherson, C., Layman, D., Maas, J., Jaeger, S., Walker, R., Walle, K., Sekhon, M., Becker, M.C., O'Laughlin, M.D., Schaller, M.E., Fewell, G.A., Delehaunty, K.D., Miner, T.L., Nash, W.E., Cordes, M., Du, H., Sun, H., Edwards, J., Miner, T.L., Lawar, R., Courtney, L., Kalicki, J., Ozersky, P., Bradshaw-Cordum, H., Ali, J., Andrews, S., Isak, A., Wanbrunt, A., Nguyen, C., Du, M., Hou, S., Tomlinson, C., Harkins, R., Harris, A., Strong, C.M., Hou, S., Tomlinson, C., Dauphin-Kohlberg, S., Kozlowicz-Reilly, A., Leonard, S., Rohlfing, T., Strowmatt, C., Latrellle, P., Miller, N., Johnson, D., Murray, J., Kocesner, J.P., Wendl, M., Abbott, A., Minx, P., Maupin, R., Wallis, J.W., Weessner, J.P., Wendl, W., Sphultz, B.R., Wallis, J.W.,

USA USA USA Louis Spieth, J., Bieri, T.A., Nelson, J.O., Berkowicz, N., Wohldmann, P.E., Cook, L.L., Hickenbotham, M.T., Eldred, J., Williams, D., Bedell, J.A., Maria, B.R., Clifton, S.W., Chissoe, S.L., Marra, M.A., Raymond, C., Haugen, E., Gillett, W., Zhou, Y., James, R., Phelps, K., Iadanoto, S., Bubb, K., Simms, E., Levy, R., Clendenning, J., Kaul, R., Kent, M.J., Furey, T.S., Baertsch, R.A., Brent, M.R., Keibler, E., Flicek, P., Chinwalla, A.T., Gish, W.R., Eddy, S.R., McPherson, J.D., Olson, M.V., Eichler, E.E., Green, E.D., Waterston, R.H. and Wilson, R.K. Washington Missouri 63108, 63108, Department of Genetics, Washington Park Avenue, St. Louis, Missouri 63108, Direct Submission Submitted (27-JUN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. 1 MO 63108, USA Materston, R.H. Sequencing Center, Washington 4444 Forest Park Parkway, St. Washington Direct Submission
Submitted (30-JAN-2004) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63
On Feb 16, 2001 this sequence version replaced gi:11597125. 2 (bases 1 to 136901)
Bauer, H., Haakenson, B. and Nguyen, C.
The sequence of Homo sapiens BAC clone RP11-95P9
Unpublished (2001)
3 (bases 1 to 136901) Department of Genetics, Park Avenue, St. Louis, 424 (6945), 157-164 (2003) Submitted (16 FEB-2001) Genome University School of Medicine, MO 63108, USA Submitted (09-MAY-2001) University, 4444 Forest 6 (bases 1 to 136901) Submitted (29-APR-2003) University, 4444 Forest 7 (bases 1 to 136901) (bases 1 to 136901) Direct Submission Direct Submission Direct Submission Waterston, R.H. Waterston, R. Waterston, 12853948 Nature REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL AUTHORS TITLE JOURNAL AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE REFERENCE REFERENCE

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

Center: Washington University Genome Sequencing Center

Web site: http://genome.wustl.edu Contact: sapiens@watson.wustl.edu Center project name: H_NH0095P09 Summary Statistics

Center code: WUGSC

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all acquencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

and The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Exic D. Green, Director). John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information MAPPING INFORMATION:

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95497 AAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCAGGAAGCAGTTAGAGTGGT
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/rpt_family="MER1_type"

17513. 17684

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17513. 17684
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20943. 20966
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15457 . 15494
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15515 . 15552
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15997. 16043
/rpt_family="(CA)n"
16497. 16517
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Location/Qualifiers
                                                                                                                    SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries Genomics 51:1-8. The clone may be obtained either from and coworkers at http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                    about the map position of this sequence, see
http://www.nhgri.nih.gov/DIR/GTB/CHR7 , send
mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu
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9247_ 9288
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9289_ 9399
/rpt_family="MalR"
9412_ 9494
/rpt_family="MalR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol type="genomic DNA"
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8004. 8064
/rpt_family="(TATG)n"
8067. 8206
/rpt_family="MaLR"
9047. 9246
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/rpt. family="(TAA)n"
14453. .14659
/rpt. family="MIR"
15191 . .15248
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/clone_lib="RPCI-11"
545. 1149
/rpt_family="L1"
1195. 1380
/rpt_family="L1"
1533. 1790
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4398, ,14424
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rpt_family="AT_rich"
829. .7985
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/rpt_family="Alu"
10815. .10909
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0530. .10814
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Score 571, DB 9; Length 136901; Pred. No. 5.4e-169; 0; Mismatches 40; Indels 0;

89.9%; 93.7%;

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Submitted (19-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, Caudmitted (19-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Oct 2, 2001 this sequence version replaced gi:14702155.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Emis, EMBL; Sw:, SWISSRROT; Tr:, TREMBL; WORMPEP; Information on the WORMPEP here.
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VECTOR: pBACc3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-134K1 It may be shorter because we sequence overlapping
sections only once, except for a short overlap.
The true right end of clone RP11-134K1 is at 89728 in this
sequence. The true right end of clone RP11-60C15 is at 2000 in this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL583805 B9728 bp DNA linear PRI 29-SEP-2001
Human DNA sequence from clone RPI1-134K1 on chromosome 9, complete
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 89728)
                             481 AGAGCACAGCGGGAGGGACAAGGATATAAACCCAGGCATTCGAGCGGCAACGG
                                                                                                                                                                                                                                     57416 AGAGCACAGTGGGAGGACAAGGATTGCAATATAAACCCAGGCATTCGAGCCAGCAACGG
                                                                                                  ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
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       GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
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AL583805 AC051658
AL583805.7 GI:15865009
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Submitted (29-AUG-2002) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
On Aug 29, 2002 this sequence version replaced gi:14625082.
Location/Qualifiers
1. 176188
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                                                                                                                                                                                                                                ACO68898 176188 bp DNA linear PRI 29-AUG-2002
Homo sapiens chromosome 10 clone RP11-534L6, complete sequence.
ACO68898
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 176188)
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Pred. No. 1.6e-167;
0; Mismatches 41;
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Matches 591; Conservative 0
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Direct Submission
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 112405)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                88.9%; Score 564.6; DB 9;
llarity 94.2%; Pred. No. 5.4e-167;
Conservative 0; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  601 ATTAAATCTTGCAACTGAAAAAAAAAAAAAAAAAAA 635
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                         .. .89728
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cocation/Qualifiers
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Homo sapiens
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Alabrooks, S. L., Amaratunge, H. C., Are, J. R., Ayele, M., Banks, T., Barbarda, C., Burch, P., Burket, C., Burch, B., Bankon, B., Barbarda, M., Britan, B., Barbarda, C., Burch, P., Burket, C., Burch, M., Britan, M., Davis, C., Cox, C., Coyle, M. D., Dathorne, S. R., David, R., Davis, C., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, Z., Chowdhry, I., Christopoulos, C., Davis, D., Davis, M., Davis, C., Cox, C., Dayen, R., Davis, C., Davis,

repeat_region

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INFORMATION: http://www.hgsc.bcm.tmc.edu/ or emailgc-help@bcm.tmc.edu
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES: STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts:

Ropeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences. Genes and Region of sequence similarity (axpect < 18-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found E

http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht

FEATURES

Location/Qualifiers

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/chromosome="3" clone="RP11-3J2"

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complement (914. 1221)
/rpt_family="AluSg"
complement (1222. 1808)
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complement (2045. 1298) rpt_family="LIME" 454. .2811 repeat_region repeat_region

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complement (63377. .6630)
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14620, 14933 / /rpt_family="AluSg" complement(15183, 15254) family="LiPA16"
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complement(12489. rpt_family="MIR" rpt_family="L1" 1295. .11658 family="L2" 'rpt_family="LiPH complement(10830 rpt_family=_ 18793. .19462 .10818 18635 rpt_f 0754. repeat_region repeat_region

Length 112405; Score 560.2; DB 9; Pred. No. 1.4e-165; 38; 0; Mismatches 88.2%; 93.8%; Query Match
Best Local Similarity 93.8
Matches 594; Conservative 67640

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CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA

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an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at one
                                                                                                                                                          subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
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ilarity 94.0%;
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DNA sequence and comparative analysis of chimpanzee chromosome 22

DNA sequence and comparative analysis of chimpanzee chromosome 22

DNA sequence and comparative analysis of chimpanzee chromosome 22

E (bases 1 to 17914)

E (bases 1 to 17914)

E Hattori,M., Toyoda,A., Watanabe,H., Taylor,T.D., Kuroki,Y.,

Direct Submission

E vijyama,A. and Sakaki,Y.

Direct Submission

Submitted (12-MAY-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Subhiro-chou,Tsurumi-ku, Vokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

The Chimpanzee Chromosome 22 Sequencing Consortium consists of:

*Chimpanzee Chromosome 22 Sequencing Consortium consists of:

*Chimpanzee Chromosome 22 Sequencing Consortium consists of:

*Chimpes National Human Genome Center at Shanghai, Shanghai, China;

*GBF, Dept. of Genome Analysis, Braunschweig, Germany; *Institute Center of Molecular Blotechnology, Jena, Germany; *KRIBB Genome Research
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Pan troglodytes chromosome 22 clone:RP43-179P23, map 22, complete
sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                        541 CAACCCCTTTGGGTCCCCTCCTTTGTATGGGCGCTCTGTTTTCACTCTATTCACTCT
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                                                                                           <u> ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG</u>
                                                                                                                                                                                                                                                                   AGAGCACAGCGGGACGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
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263 bases at least Q30
35 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68180 ATTAAATCTTGCAACTGCAAAAAAAAAAAAAA 68212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         601 ATTAAATCTTGCAACTGAAAAAAAAAAAAA 633
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Center: RIKEN Genomic Sciences Center
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BS000045.1 GI:37537312
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Consensus quality:
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169125 CAPATAGTTCTTCAPATGGAGCCCCAGATGCAGTCCATGACTAAGATCCACGGGGCCC 169066
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The RPCI-43 chimpanzee BAC library was prepared from DNA isolated from the blood of a single male chimpanzee using published protocols (Osoegawa, K. et al. Genomics 52:1-8). The DNA from the chimpanzee ('Clint') was obtained from the Yerkes Primate Center in Atlanta. The library was prepared by Baoli Zhu, Chung Li Shu, Kazutoyo Osoegawa, Evan Eichler & Pieter J de Jong. The library characteristics are described at
                                                                                                                                                                                                                                                                                                                                                                                 YECTOR: pBACE3.6

The CHORI-251 chimpanzee BAC library was prepared from DNA isolated from the blood of a single male chimpanzee using published protocols (Osoegawa,K. et al. Genomics 52:1-8). The DNA from the chimpanzee ('Clint') was obtained from the Yerkes Primate Center in Atlanta. The library was prepared by Baoli Zhu, Chung Li Shu, Kazutoyo Osoegawa, Evan Eichler & Pieter J de Jong. The library http://www.chori.org/bacpac/chimpanzee251.htm.

The clone may be obtained from Pieter J de Jong and coworkers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VECTOR: DIARBAC2.1
The PTB1 chimpanzee BAC library was prepared from DNA isolated from cultured cells established from the blood of a single male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (http://www.gsc.riken.go.jp).
VECTOR: pkS145
The PTF22 chimpanzee Fosmid library was prepared from DNA isolated
from cultured cells established from the blood of a single male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACGTGGACCC
                                                                                                                                                                                                                                                                               http://www.chori.org/bacpac/mchimp43.htm.
The clone may be obtained from Pieter J. de Jong and coworkers (http://www.chori.org/bacpac).
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/clone_lib="RPCI-43 chimpanzee BAC"
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/organism="Pan troglodytes"
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/db_xref="taxon:9598"
/chromosome="22"
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36170 CAACCCCCTTTGGGTCCCCTGCCTTTGTATGGGAGCTCTGTTTTCACTCTATTTCACTCT 36111
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Homo sapiens genomic DNA, chromosome 21q, section 18/105.
AP001674 AL163219 BA000005
AP001674.1 GI:7768666
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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         Length
                                           Indels
     Score 556.6; DB 9;
Pred. No. 2.1e-164;
0; Mismatches 39;
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nilarity 93.7%;
Conservative 0
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           Query Match
Best Local Similarity
Matches 580; Conserv
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El (bases 1 to 114019)

Es Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 174,019 genomic DNA of 21q21.1-q21.2

Li Published Only in DataBase (2000)

E (bases 1 to 174019)

E Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Eujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission

E vijyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission

Submitted (33-MAR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato, Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@sec.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9923,
                                                                                                                                                                                                                                                                                                                                                                            168766
                                                                                                     168946
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                                                                                    168885 AGGACTAGCTGGATTTCCTAGGCCAACTAAGAAGCCCTAAGCCTAGATGGGAAGATGAGAAGATGA
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Battori, M., Fujiyama, A., Taylor, T.D., Watanabe, H., Yada, T.,
Battori, M., Fujiyama, A., Taylor, T.D., Watanabe, H., Yada, T.,
Bark, H.S., Tayoda, A., Tahli, K., Totori, D.K., Soeda, E.,
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Hennig, S., Riesselmann, L., Dagand, E., Wehrmaeyer, S., Borzym, K.,
M. M. Maretic, D., Francis, F., Lehrach, H., Reinhardt, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-APR-2000) The Chromosome 21 Mapping and Sequencing Submitted (10-APR-2000) The Chromosome 21 Mapping and Sequencing Consortium: * RIKEN Genomic Sciences Center, Human Genome Research Group * Institute of Molecular Biotechnology, Genome Analysis * Keio University School of Medicine, Dept. of Molecular Biology * Genome Analysis * Max-Planck Institute for Molecular Genetics (addresses see Delow)
On May 30, 2000 this sequence version replaced gi:771721.
* RIKEN Genomic Sciences Center, Human Genome Research Group, * Sagamihara, 228,8555, Japan.
  Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and
Yaspo,M.L.
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* Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail:

Info:genome@gbf.de

* URL: http://genome.gbf.de/
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Beutenbergstrasse 11, D-07745 Jena, Germany,
* e.mail: gscj-submit@genome.imb-jena.de
* URL: http://genome.imb-jena.de/
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* e.mail: nshimizu@dmb-med.keio.ac.jp
* URL: http://www.dmb.med.keio.ac.jp/
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 149755)

Rattori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 149,755 genomic DNA of 18q21

Leblished Only in DataBase (2000)

E (bases 1 to 149755)

Rattori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., B., Hattori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., S. Hattori,M., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission

Listana,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission

Lomited (24-MAR-2000) Massahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1.15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan

1.15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan

(B-mail:hattoriogsoc.riken.go;p, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923; Fax:81-42-778-9924)
                           NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved
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Homo sapiens chromosome 18 clone RP11-762G24 map 18q21, WORKING
DRAFT SEQUENCE, 13 unordered pieces.
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HTG; HTGS PHASE1; HTGS DRAFT.
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93.7%; Pred. No. 2.3e-164;
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130456. .133619
/133720 .137416
146768 148219 contig of 1452 bp in length.
148320 149755 contig of 1456 bp in length.

* NOTE: This is a 'working draft' sequence. It currently
consists of 13 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
                                                                                                                                                               44928: contig of 44828 bp in length

44928: gap of 100 bp

82602: contig of 37674 bp in length

82102: gap of 100 bp

101344: contig of 18642 bp in length

101344: contig of 18642 bp in length

116305: gap of 100 bp

116305: gap of 100 bp

123784: contig of 7479 bp in length

123884: contig of 6471 bp in length

130855: contig of 6471 bp in length

130855: contig of 6471 bp in length

130855: gap of 100 bp

130856: gap of 100 bp

13719: gap of 100 bp

13719: gap of 100 bp

137416: contig of 3164 bp in length

137416: contig of 4024 bp in length

141540: contig of 4024 bp in length

141540: contig of 4024 bp in length
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of 2711 bp in length
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Length 149755;

Score 551.8; DB 2; Pred. No. 6.8e-163;

86.9%; 91.8%;

Query Match Best Local Similarity

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67547 AGAGCACAGGGGGGGGGACAAGGATCAGGATATAAACCCAGGCATTCGAGCCGGCAACGG 67606
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 152980)
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HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_CANCELLED.
Homo sapiens (human)
Homo sapiens
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Homo sapiens chromosome 18, clone RP11-762G24
Unpublished
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0; Mismatches
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PRI 16-NOV-2001

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48688 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAGCTGTAAAACTA 48629
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DOE Joint Genome Institute.
Dobrict Submission
Submitted (31-AUG-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 163803)
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                                                                                                                                                      AC093531 163803 bp DNA linear PRI 16-NOV.
Homo sapiens chromosome 5 clone RP11-405L7, complete sequence.
AC093531
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* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be preserved.

* Location/Qualifiers
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Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Center project Information
Center project name: 1.12582
Center clone name: 762_6_24
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/clone_lib="RPCI-11 Human Male BAC"
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Pred. No. 6.8e-163;
0; Mismatches 52;
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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/chromosome="18"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 176425)
Sulston,J.E. and Waterston,R.
                                                     Toward a complete human genome
Genome Res. 8 (11), 1097-1108
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                                                                                                                                                                                                                          Length 163803;
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                 www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.3.
Location/Qualifiers
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Pred. No. 6.9e-163;
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                                                                                                                     /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/clone="RP11-405L7"
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al Similarity 93.2%;
577; Conservative
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Matches 57
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NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-624F4; the clone sequenced
to the right is RP11-362J3. Actual start of this clone is at base
position 1 of RP11-452N17; actual end is at base position 176425 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (30-MAY-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 5 (Dases 1 to 176425) Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
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The RPCI-11 human BAC library was made from the blood of one male donor, as described by geoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
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                                                                                                                                                                                                                                                               Louis,
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                                                                                                                                                                                                                              Washington
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                                                                                                                                                                                                                              Sequencing Center, Washing
4444 Forest Park Parkway,
2 (bases 1 to 176425)
Swearengen-Shahid, S., Meyer, R. and Dignan, G.
The sequence of Homo sapiens BAC clone RP11-452N17
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: H_NH0452N17
                                                                                                                                                                                                                              Submitted (15-JAN-2002) Genome University School of Medicine, MO 63108, USA 4 (Dases 1 to 176425)
                                                                                                                                           3 (bases 1 to 176425)
Waterston, R.H.
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RP11-452N17.
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PRI 12-JUN-2002 sequence.

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176425 bp Homo sapiens BAC clone RP11-452N17 AC107075

DEFINITION

ACCESSION VERSION KEYWORDS

AC107075.4 GI:21263352

sapiens (human)

Homo

ORGANISM

SOURCE

DNA

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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161008 CAPATCGTTCTTCAPATGGAGCCCCAGATGCAGTCCATGACTAAGATCTACGTGGACCC 160949
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86.9%; Score 551.8; DB 9;
Best Local Similarity 92.8%; Pred. No. 6.9e-163;
Matches 593; Conservative 0; Mismatches 37;
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Polymorphisms exist between AC110086 and AC107075. Data from AC110086, AC116626 and AC018872 was used to finish AC107075. Location/Qualifiers
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7966. 8026

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9; Gaps

Indels

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VECTOR:
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http://www.sanger.ac.uk/HGP/Chr6
http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (05-MRR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequestesdeanger.ac.uk
On Nov 20, 2000 this sequence version replaced gi:11125403.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequence with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Ems. EMBL; Sw.; SWISSPROT; Tr.; TREMBL; WP.; WORMPEP: Information on the WORMPEP database can be found at
                                                                                                                                                                   160648 GGAGAGCTCACTAAATGCTAATTAGGCAACAACAAGAGGGTAAAGAAATAGCCAATCACC 160589
                                                                                                                                                                                                                                                             160708 GCTTCCATCTTTAAACACGGGCTTACAACTTAACTCACACATGACCAATCAGATAGTAA 160649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL139090 128468 bp DNA linear PRI 12-APR-2001
Human DNA sequence from clone RPI1-12B13 on chromosome 6 Contains
STSs and GSSs, complete sequence.
                                                                                                                                                                                                                                    531
                                                                                                                                                                                                                                                                                                                               591
                                              GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCA----- 412
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Catarrhini, Hominidae, Homo.
                                                                                                                                        413 -GAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATC
                                                                                                                                                                                                                                  472 TATTGCCTGAGAGCACAGGGGAGGACAAGGATCGGGATATAAAACCCAGGCATTCGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                           592 TITCACICIATIAAAICIIGCAACIGAAAAAAAAAAA 630
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Mammalia; Eutheria; Primates;
1 (bases 1 to 128468)
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Homo sapiens
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Direct Submission
                                                                                                                                                                                                                                                                                                                                        532
                                                        361
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KEYWORDS
SOURCE
ORGANISM
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AL139090/c
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18040 . 18346

/note="LiMEc repeat: matches 2106 . 2409 of consensus"

18471 . 18874

/note="LiMEc repeat: matches 1469 . 1910 of consensus"

complement(18475 . 18995)

/note="match: GSS: Em:AQ755181"

18938 . 19072

/note="match: repeat: matches 1243 . 1377 of consensus"

19459 . 19514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7552. 17740
note="LIMEc repeat: matches 2408. 2260 of consensus"
7741. 18039
note="AluSx repeat: matches 1. 299 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="LIPAS repeat: matches 5526. .6143 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="LIME3 repeat: matches 4094. .4381 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146. .8805
note="L1ME3 repeat: matches 4381. .6140 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7077. .17544 matches 2710. .3168 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                711. .15846
note="L1PA6 repeat: matches 11. .6143 of consensus"
5826. .16269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="MER41B repeat: matches 114. .601 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20321. .20675
Totte="LTR16B repeat: matches 97. .464 of consenBus"
20952. .21137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="12 repeat: matches 1693. .2089 of consensus" 3497. .3668 /note="MER20 repeat: matches 16. .188 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                      /note="12 repeat: matches 2574. .2704 of consensus"
2290. .2509
/note="12 repeat: matches 2098. .2328 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="MER5A repeat: matches 3. .186 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat: matches 64. .153 of consensus"
                                                                                                                                                                                                                                                                                                                                                                .966 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .4135 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="AluJo repeat: matches 120. .307 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="26 copies 2 mer aa 71% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="28 copies 2 mer ca 96% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5826, ,16269
note="LIM4 repeat: matches 3692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (4521. .5085)
/note="match: GSS: Em:AQ421033"
complement (4571. .5086)
/note="match: GSS: Em:AQ883615"
complement (4633. .5083)
/note="match: GSS: Em:AQ812769"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="match: GSS: Em:AQ544837"
085. .6174
                                                                                                                                                                                                                  'note="match: GSS: Em:AQ609536"
                                                                                                                                                                                                                                                                     Em: AQ704228"
                                                                                                                                                                                                                                                                                                                                                                   /note="LTR5 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                     Em: B75711"
                                   . .128468
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/clone="RP11-12B13"
                                                                                                                                                                       clone_lib="RPCI-11.1"
location/Qualifiers
                                                                                                                                                                                                                                                                     'note="match: GSS:
                                                                                                                                                                                                                                                                                                                     /note="match: GSS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2976. .3352
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.6184 of consensus"

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note="HERV17 repeat: matches 8244. .8523 of consensus" 3811. .38137 repeat: matches 1651. .5933 of consensus" note="HERV17 repeat: matches 1651. .5933 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0490. .41321

note="Limix" repeat: matches 257. .780 of consensus"

1056. .41321

note="Limix" repeat: matches 5261. .6131 of consensus"

1354. .41655

1071. .42279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "note="LiMEC repeat: matches 2373. .3522 of consensus"
19436   .50712
"note="LiMD2 repeat: matches 5056. .6333 of consensus"
complement (50811. .51360)
innote="matches" GSS: Em: Ap536659"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="LipA3 repeat: matches 2255. .6146 of consensus"
6710. .57178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .4645 of consensus"
                                                                                                                                                                   73482. .26261

7note="LiPA3 repeat: matches 5. .776 of consensus"

86257. .31504

16157. .31504

16161. .32312

7note="LiM4 repeat: matches 3918. .4608 of consensus"
                                                                                                                                                                                                                                                                         2398. 32850
note="LIM4 repeat: matches 4626. .4909 of consensus"
12799. 32963
'note="FRAM repeat: matches -2. .162 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="L1M4 repeat: matches 2169. .2266 of consensus"
3366. .43774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="MLTIC repeat: matches 1. .463 of consensus" 7746. .57868 note="MER33 repeat: matches 202. .323 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="HBRV17 repeat: matches 1. .1836 of consensus"
9958. .40489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="MER44C repeat: matches 1. .727 of consensus"
8555. .58752
                                                                                    consensus"
                                                                                                                                                                                                                                                                                                                                                   13151. .33174

"note="12 copies 2 mer tt 95% conserved"

13176. .33500

"note="LTR17 repeat: matches 1. .326 of consensus"

13501- "33791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="MER33 repeat: matches 1. .202 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="AluSg repeat: matches 1. .307 of consensus"
59630. .60070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="AluSx repeat: matches 1. .303 of consensus"
3255. .43365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="MSTA repeat: matches 1. .426 of consensus"
              consensus"
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8017. .49417
              matches 90.
                                                 Em: AQ027280'
23421. .23472
/note="MIR repeat:
24395. .24791
                                               note="match: GSS:
4638. .24848
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Catarrhini, Hominidae, Homo.
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Submitted (14-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                               33791 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATTGAAACTGTAAAACTA
                                                                                                                                                                                                                                                                                          481 AGAGCACAGCGGGAGAGACAGGATATAAACCCAGGCATTCGAGGCGGCAACGG
                                                                                                                                                                                                                                                    33671 CT-GATCAACCTCCTAGCCCATGCTCCAATGTTAATGACATTGAAGGCACCCCTCCCGAG
                                                                                                                                                                                                                                                                            GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCGGACCAATCAGAGGAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                            421 ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
                                             .6164 of consensus"
                                                                                                                                                                                                                               CTGGACCGGCCTGCTAGCCCCATGCTCGATGACATTGAAGGCACCCCTCCCGAG
                                                                                                                                                                                                                                                                                                                                                                            AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
                                                                                                                               1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA
                                                                                                                                                                               61 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
                                                                                                       Gaps
                                                                                Length 128468;
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                                                                                                       Indels
          59956. .60646
/note="match: GSS: Em:B82923"
61550. .61582
/note="LIME2 repeat: matches 6133.
61583. .62103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="L1MB3 repeat: matches 5737.
                                                                               Query Match 86.8%; Score 551.4; DB 9; Best Local Similarity 93.9%; Pred. No. 8.8e-163; Matches 596; Conservative 0; Mismatches 36;
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Mammalia; Eutheria; Primates;
1 (bases 1 to 140756)
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                  requence constructions becauser. July 2011 17, 2001 this sequence version replaced gi:13751261.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; We., MORMPEP; Information on the WORMPEP; Heard of the contraction of the WORMPEP; Information on the WORMPEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMPORTANT: This sequence is not the entire insert of clone RP11-456B18 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-456B18 is at 140756 in this sequence. The true left end of clone RP11-78L16 is at 68441 in this sequence. The true right end of clone RP11-108H9 is at 100 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.anger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 happing Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chri3 RP11-456B18 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.choriorg/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="LIME3 repeat: matches 6002. .6146 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="HERV23 repeat: matches 993. .1056 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="LTR16A repeat: matches 203. .442 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          matches 483. .677 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          matches 410. .465 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="MER41C repeat: matches 1. .131 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               623. .9732
note="LTR1 repeat: matches 675. .785 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MLT2D repeat: matches 1. .486 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="LOR1b repeat: matches 1. .461 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           matches 6. .203 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1830. -2326
/note="LORIa repeat: matches 1. .497 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="LTR8 repeat: matches 1. .691 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         matches 454. .539 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  copies 2 mer gt 94% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mer tt 59%
          requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="13"
/clone="RP11-456B18"
/clone_lib="RPCI-11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       000. .6083
note="MER34 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          992. .9049
note="MER4D repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="LTR29 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="MER4D repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="110 copies 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .140756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     932. .3965
note="17 co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .6171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . .5893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seguence.
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                                       COMMENT
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note="MSTC-internal repeat: matches 2. .1651 of consensus"
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31813. .32243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="L1MC4 repeat: matches 6629. .7089 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thote="Limit" repeat: matches 5745. .6199 of consensus" 70913. .21222 / Thote="Limit" repeat: matches 5277. .5594 of consensus" 70013. .21303. .21303. .21303. .21304. .21309. .21304. .21309. .21304. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309. .21309.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat: matches 4726. .5242 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .354 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MER66A repeat: matches 163. .478 of consensus"
16903. .17014
/note="MER54B repeat: matches 3. .115 of consensus"
17195. .17491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11645. .21984
hote="LTR19B repeat: matches 55. .393 of consensus"
.2081. .22583
hote="LIMD2 repeat: matches 4726. .5242 of consensus"
.3498. .23784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MER54B repeat: matches 585. .789 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="MERS4B repeat: matches 112. .278 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         matches 283. .341 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8120. 19291
note="LIP repeat: matches 1726. .2897 of consensus"
                                                                                                                                                                                                                                                                                                     'note="MER4D repeat: matches 396. .973 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="Alusx repeat: matches 20. .311 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="AluJb repeat: matches 1. .305 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "note="MERGGA repeat: matches 1. .69 of consensus" 16570. .16629 ropeat: matches 283. .341 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        matches 1. .295 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .151 of consensus"
                                                                                                                                                                                                                        note="MER4D repeat: matches 1. .234 of consensus"
[2164. .12767
                                                                                                                                                                                                                                                                                                                                                                               matches 1. .364 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="MIR repeat: matches 31. .238 of consensus" 15404. .25696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat: matches 1. .405 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="AluY repeat: matches 1. .297 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="THE1B-INTERNAL repeat: matches 1. .1580 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="25 copies 5 mer atttt 62% conserved"
9686. .19745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tg 95% conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .394 of
                                                                                                                                                       .144 of
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30688. 30874
/note="MER61A repeat: matches 160.
31648. 31785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="12 copies 5 mer tttaa 71%
                                                                             'note="MER67D repeat: matches 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat: matches 30.
repeat: matches 2.
                                                                                                              11249. .11332
/note="MIR repeat: matches 69.
11923. .12159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3873. .24169
note="AluSg repeat:
                                                                                                                                                                                                                                                                                                                                                                                       /note="THE1B repeat:
13222. .14798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5832. .26218
note="MSTC re
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note="L1PB2 r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8710. .29043
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Size (bases 1 to 16736)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barran, N., Beckerly, R., Béda, F., Anderson, S., Baldwin, J., Barran, N., Beckerly, R., Béda, F., Anderson, S., Baldwin, J., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Gooke, P., DeArellano, K., Dewar, K., Lonino, M., Doyle, M., Farestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Farreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Mardulad, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Mardulad, J.C., Johnson, R., Jones, C., Liu, G., Locke, K., Madonald, P., Marquis, M., McEwan, P., McGurk, A., McRenan, K., McMens, L., Mortow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnall, P., Olivar, T.M., Peterson, K., Fleire, R., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Stojanovic, N., Subramanian, A., Talamas, J., Stange-Thomann, D., Ye, W.J., Tirrell, A., Vassiliev, H., Viel, R., Wu, X., Wyman, D., Ye, W.J., Jircell, A., Vassiliev, H., Viel, R., Wu, X., Wyman, D., Ye, W.J., Jircet, Submission

All repeats were identified using RepeatMasker: html

Submitted (20-JAN-2000) Whitehead Institute/MIT Center for Genome Research

Center: Whitehead Institute/ MIT Center for Genome Center: Mithehead Institute/ MIT Center for Genome Center: Mithehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                             69776
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACO21774 16736 bp DNA linear HTG 30-MAR-2000
Homo sapiens clone RP11-13C18, WORKING DRAFT SEQUENCE, 10 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                           AGAGCACAGCGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
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Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: project Information
Center project name: 13.15
Center clone name: 13.215
Center clone name: 13.75
Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 16780 bases at least Q40
Consensus quality: 16780 bases at least Q30
Consensus quality: 16588 bases at least Q20
Insert size: 170000; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 167366)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-13C18
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC021774.3 GI:7341907
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                             69777 GTTAAATCTTGCAACTGCA 69795
                                                                                                                                                                                                                                                                                   601 ATTAAATCTTGCAACTGAA 619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18708. .48806
/note="AluJo/FRAM repeat: matches 197. .297 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09
                                                                                                                                                                                                                                                                    .6152 of consensus"
                                                                                                                                                                                                                                                                                                                                            41279. .41308
/note="15 copies 2 mer aa 86% conserved"
42744. .42933
42746. .e="LiMAB repeat: matches 6064. .6256 of consensus"
42973. .43275
/note="AluSx repeat: matches 1. .303 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69181 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGACTCTTCCAGAATTAAAACTGTAAAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACGTGGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGACCGGCCTGCTAGCCCCATGCTCAATGACATTGAAGGCACCCCTCCCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTTCCAGAATCAAAACTGTAAAACTA
                                                                                                                                            34465. .34825
/noce="THBLC repeat: matches 1. .360 of consensus"
/noce="MER67C repeat: matches 202. .403 of consensus"
/note="MER67C repeat: matches 6076. .6152 of consensus"
/note="LiPAl2 repeat: matches 6076. .6152 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="LIME repeat: matches 974. .1253 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .448 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52250. .52349
Thote="MIR repeat: matches 131. .228 of consensus"
52696. .52996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :5196. .45584
'note="MLT2B repeat: matches 2. .399 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="THEIC repeat: matches 1. .370 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="AluSg repeat: matches 1. .293 of consensus"
                                            of consensus"
                                                                                                                                                                                                                                                                                                                  note="AluY repeat: matches 1. .308 of consensus"
                                                                                        'note="THEIC-internal repeat: matches 3. .1651 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 140756;
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Anote="Limmer repeat: matches 2274. .2369 of

30637. .50927
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Mote="87 copies 2 mer ta 77% conserved"

15800. .45851

Mote="MLTZB repeat: matches 394. .448 o

18118. .48487
                                    /note="THEIC repeat: matches 1. .371
32824. .34464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 551.4; DB 9;
Pred. No. 8.9e-163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (43560, .43991)
/note="match: STS: Em:HSPH07E5"
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ilarity 94.3%;
Conservative
                                                                                                                          consensus"
34465. .34
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Best Local Similarity
Matches 584; Conserv
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Homo sapiens
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ACCESSION
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AL607153
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                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 167366;
Insert size: 166466; sum-of-contigs
Quality coverage: 4.8 in Q20 bases; agarose-fp
Quality coverage: 4.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                            273 1372: contig of 1272 bp in length 1372: gap of 100 bp 4088: contig of 2716 bp in length 1388: gap of 100 bp 6500: contig of 2716 bp in length 189 6500: contig of 2312 bp in length 6500: contig of 2312 bp in length 6501 15485: contig of 8885 bp in length 15486: contig of 8885 bp in length 15885: gap of 100 bp 738 27737: gap of 100 bp 738 3958: contig of 12221 bp in length 1959 4058: gap of 100 bp 738 3958: contig of 14560 bp in length 1619 64718: gap of 100 bp 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .167366
/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="texon:9606"
/clone="RP11-13C18"
/clone="RP11-13C18"
/lone="AP72"
1. .1272
1. .1272
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6601. 15485
/note="assembly_fragment"
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40059. .54618
//note="assembly_fragment"
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/note="assembly_fragment"
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123333. .167366
/note="assembly_fragment"
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/note="assembly_fragment"
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6996 CAATCCCCTTTGGGTCCCCTCC--TTGTATGGGAGCTCTGTTTTCACTCTATTTCACTCT 6939
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
Direct Submission
Submitted (18-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, Submitted (18-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@senger.ac.uk clonerequestGesnger.ac.uk
On Oct 5, 2001 this sequence version replaced gi:15962724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 481 AGAGCACAGGGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
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                                                                                                                                                                                                                                                                                                                                                                                                           GCATCCACCTCAAACATGGGGCTTGCAACTTAGCTCACACCGACCAATCAGAGGCTC
                                                                 CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
                                                                                       GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
                                                                                                                                                                            CATCAGCCAACCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC
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Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 183433 bases at least Q40
Consensus quality: 183439 bases at least Q30
Consensus quality: 183441 bases at least Q20
Insert size: 183499; sum-of-contigs
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Homo sapiens chromosome 13 clone RP13-276D12.
AL607153
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Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
Contact: humquery@sanger.ac.uk
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HTG; HTGS PHASE2; HTGS_CANCELLED.
Homo sapiens (human)
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NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
                                                   164211 bp DNA linear HTG 13-JUL-2000
HOMO sapiens chromosome 18 clone RP11-732P12 map 18q21, WORKING
AP002790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (11-JUL-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, UKL.http://hgp.gsc.riken.go.jp/,
                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarthin; Hominidae; Homo.

I (Dases I to 16421)

Hattori,M. 1shii,K. Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totcki,Y., Watanabe,H. and Sakaki,Y. Fujiyama,A., Yada,T., Totcki,Y., Watanabe,H. and Sakaki,Y. Published Only in DataBase (2000)

2 (bases I to 164211)

2 (bases I to 164211)

Eujiyama,A., Yada,T., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totcki,Y., Watanabe,H. and Sakaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: RIKEN Genomic Sciences Center (GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: http://hgp.gsc.riken.go.jp/
Contact: http://ggsc.riken.go.jp/
Contact: http://ggsc.riken.go.jp/
Contact: project Information
Center project name: Humbraft18
Center project name: RR11-732P12
Center clone name: RR11-732P12
Center clone name: RR11-732P12
Center clone name: RR11-732P12
Center project name: RR11-732P12
Cen
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Consensus quality: 154344 bases at least Q40
Consensus quality: 159150 bases at least Q30
Consensus quality: 161200 bases at least Q30
Insert size: 162311; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (B-mail:hattori@gsc_riken.go.jp, ŬRL:ht
Tel:81-42-778-9923, Fax:81-42-778-9924)
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
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                                                                                * NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* In 183499: contig of 183499 bp in length.
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Insert size: 179011; 5.6% error; agarose-fp
Quality coverage: 12.84x in Q20 bases; sum-of-contigs Quality
coverage: 13.23x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 183499;
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Pred. No. 9.4e-163;
0; Mismatches 31;
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94.3%;
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CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC 120
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                                                                                                                                                                                                                                                                                                                                                      Score 550.2; DB 2;
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Best Local Similarity 91.7%;
Matches 582; Conservative
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    NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                     28606: contig of 28606 bp in length 28706: gap of 100 bp 55973: contig of 27267 bp in length 56073: gap of 100 bp 73701: contig of 17628 bp in length 73801: gap of 100 bp 92513: contig of 18712 bp in length 92513: contig of 18712 bp in length 102771: gap of 100 bp 102771: gap of 100 bp 111253: contig of 8982 bp in length 111353: contig of 8882 bp in length 112057: contig of 8814 bp in length 120267: contig of 814 bp in length 120267: contig of 814 bp in length 120267: gap of 100 bp
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of 4379 bp in length
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of 2599 bp in length
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Length 164211;

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240

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Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J. Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vasilliev, H., Viel, R., Vo, A., Milson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                  Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 30, 2002 this sequence version replaced gi:21700673. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome Research
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complement(1425. .1557)
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3962. .9273
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Birren, B., Linton, L., Nusbaum, C., Lander, G., Beda, F., Boduslavkiy, L., Budwin, J., Barna, N., Barket, G., Campoplano, A., Caerle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Frreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karatas, A., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McZarthy, M., McEwan, P., McGwrna, K., Mengeleres, R., Mardy, T., Naylor, J., Mihova, T., Miranda, C., Menga, V., Morrow, J., Miranda, C., Pollara, V., Mormon, C.H., O'Connor, T., O'Connor, T., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Frander, B., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Vollara, V., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Vollar, J., Woll, R., Wu, X., Wyman, D., Ye, W. J., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Wilson, B., W
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Universe Submitted (122-ARP-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

1 (bases 1 to 167843)

1 (bases 1 to 167843)

2 Sirren, B., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farco, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Rarde, P., FitzGerald, M., Gage, D., Galagan, J., Rartas, A., Kells, C., Linger, I., Johnson, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Micol, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Micol, R., Matthews, C., Murphy, T., Naylor, J., Naron, C., Micol, R., Norbu, C., Norman, C., Phunkhang, P., Pierre, N., Raymon, C., Norlo, C., Norman, C., Roman, J., Roy, A., Schauer, S., Schuback, R., Seaman, S., Semen, S., Senter, P., Semen, S., Schauer, S., Schuback, R., Seaman, S., Sewery, P., Rage, S., Theodore, J., Topham, R., Travers, M., Vassiliev, H., Zamber, L., Zimmer, A. and Zody, M.

Direct Submission
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Submitted (06-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 167843)

S Birren, B., Nubbau, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barrata, J., Chang, J., Chazaro, B., Cheepel Y., Collymore, A., Cook, A., Cook, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, L., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, C., Landers, T., Levine, R., Lindblad, Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
                                                                        ACUDEBUL 167843 bp DNA linear PRI 30-JUL-2002
Homo sapiens chromosome 18, clone RP11-120K19, complete sequence.
AC064801
                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                               Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 18, clone RP11-120K19
Unpublished
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Human chromosome 14 DNA sequence BAC R-30513 of library RPCI-11
from chromosome 14 of Homo sapiens (Human), complete sequence.
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1 (bases 1 to 18652)

Heilig,R., Petti,C.J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P., Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C., Gyapay,G., Saurin,W. and Weissenbach,J.

Sequencing of the human chromosome 14

Unpublished

2 (bases 1 to 180523)
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Direct Submission
Submitted (01-AUG-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
On Aug 23, 2001 this sequence version replaced gi:12001714.
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                                                                       301 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
                                                                                                                                  481 AGAGCACAGGGGAGGGACAAGGATCGGGATATAAACCCCAGGCATTCGAGCCGGCAAACGG
                                                                                                                                                                                                                                                                                                          CAACCCCCTTTGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCACTCT
                                                                                                                                                                                                                                    421 ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATTGCCTG
GAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
               361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: Phrap; version 2.0
Quality coverage: 7.78x in.Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
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HTG; HTGS ACTIVEFIN.
Homo sapiens (human)
Homo sapiens
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                                 /rpt_family="MERSO"
complement(14240. 14530)
/rpt_family="AluJo"
1488]. .1528R
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/rpt family="AT rich"
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/rpt family="AbuJo"
complement(21102. 21388)
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complement(15654. 15794)
frpt_family="MERSA"
15935. 16489
/rpt_family="MLT2A2"
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/ Tpt family="AluSx"
Complement (17524. 17861)
/ Tpt family="LIMEd"
Complement (17998. 18430)
/ Tpt family="House"
19847. 19874
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complement(29806..30079)
/rpt_family="AluJb"
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/rpt_family="AluJb"
22940. .23062
/rpt_family="LIME3"
24066. .24354
                                                                                                /rpt_family="LTR16A1"
15290. .15645
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22657. .2001
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21693. 21985
/rpt_family="AluSx"
21986. 22149
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5031. .25348
rpt_family="AluSx"
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29217. .29290
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family="MLT1C"
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/rpt_family="AluY"
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2512. .13031
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29341. .29442
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Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burken, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Sequencing of human chromosome 15 D158146-D158117 region Unpublished

2 (bases 1 to 190565)

Rowen, L., Madan, A., Qin, S., Abbasi, N., Dors, M., Dickhoff, R., James, R., Loretz, C., Lasky, S., Madan, A., Prescott, S., Ratcliffe, A., Shaffer, T. and Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (25-APR-1999) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA (bases 1 to 190565) Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Barke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Pate, D., and Hood, L.
                                                                                                                                                                                                                                                                                                                                                    AC007374 190565 bp DNA linear PRI 27-MAR-2001
Homo sapiens chromosome 14 clone RP11-325L17 map 14q31, complete
sequence.
                               1016
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                                                                                          Direct Submission
Submitted (27-MAR-2001) Multimegabase Sequencing Center, Institute
Stor Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
98105, USA
On Mar 27, 2001 this sequence version replaced gi:8247780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                   1077 cracccrcrrriegerccccrcccrrreraregeaecrcagr-----rrrcacrcr
                                                                      481 AGAGCACAGCGGGAGGACAAGGATCGGGATATAAACCCCAGGCATTCGAGCCGGCAACGG
421 ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
                                                                                                                                              rGTATGGGCGCTCTGTTTTCACTCTATTTCACTCT
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985. .1035
                                                                                                                                                                                                                                            1127 ATTAAATCTTGCAACTGCAAAAACAAACAAA 1161
                                                                                                                                                                                                                         601 ATTAAATCTTGCAACTGAAAAAAAAAAAAAAA 635
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Identified using the e-PCR software (G. Schuler)"
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23437 ACTAAAATGCTAATTAGGCAAAAACAGGAGGTAAAGAAATAGCCAATCATCTATCGCCTG 23496
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Human chromosome 14 DNA sequence BAC C-2547L24 of library CalTech-D from chromosome 14 of Homo sapiens (Human), complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P., Brottier, P., Cattolico, L., Barbe, V., Pelletier, E., Artiquenave, F., Levy, M., Escemberg, R., Brulb, T., deBerardinis, V., Cruaud, C., Gyapay, G., Saurin, W. and Weissenbach, J. Seguencing of the human chromosome 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (04-MAY-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
On Jun 3, 2000 this sequence version replaced gi:7406569.
                                   540
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Downstream BAC (overlapping the SP6 end) : R-895M11 (AC=AL133153)
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Quality coverage: 7.44x in Q20 bases; sum-of-contigs
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Center code: GS
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                                                                                                                      23557 CTACCCTCTTTGGGTCCCCTCCCTTTGTATGGGAGCTCAGT-
                                                                                                                                                                                635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
                                                                                                                                                                /organism="Homo sapiens"
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larity 92.9%; Pred. No. 5.4e-162;
Conservative 0; Mismatches 35;
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55163. 55242
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110860. 110875
/note="low quality data"
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116230. 116782
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complement(11387. 11681)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences. Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:338-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission

Direct Submission

Submitted (12-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor plaza, Houston, TX 77030, USA

On Jun 26, 2002 this sequence version replaced gi:20976483.

INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email

gc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                 Submitted (26-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 112544)
                     Submitted (09-FBB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 112544)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found
                                                                                                                                                              Center, Department
of Medicine, One
                                                                                                                                                          Submitted (18-MAY-2002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA (bases 1 to 112544)
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Direct Submission
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Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Nalla, M., Morris, W., Morrow, J., Mychaleckyj, J., Naylor, J., Miloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Rid, R., Roberts, D., Roy, A., Strange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, N., Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M.

Lubmitted (22-AUG-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON Nov 10, 2000 this sequence version replaced gi:7229764.

All repeats were identified using RepeatMasker:
Smit, A.F. A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: M13, M77815; 52% of reads
Sequencing vector: Plasmid; n/a; 48% of reads
Sequencing vector: Plasmid; n/a; 48% of reads
Chemistry: Dye-primer-amersham; 2% of reads
Chemistry: Dye-primer-amersham; 2% of reads
Chemistry: Dye-terminator Big Dye; 98% of reads
Chemistry: Dye-terminator Big Dye; 98% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 199351 bases at least Q40
Consensus quality: 199351 bases at least Q30
Consensus quality: 199052 bases at least Q30
Insert size: 191678; sum-of-contigs
ANOTE: This is a 'working draft' sequence. It currently
consists of 6 contigs. The true order of the pieces
about the contigs are represented as
true of N. but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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7749: gap of 100 bp
9020: contig of 1271 bp in length
9120: gap of 100 bp
10598: contig of 1578 bp in length
10798: gap of 100 bp
12208: contig of 1410 bp in length
12308: gap of 100 bp
46811: contig of 34503 bp in length
46811: gap of 100 bp
192178: contig of 145267 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Contact: project Information
Center project name: 1.1480
Center clone name: 1.120
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/clone lib="RPC1-11 Human Male BAC"
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12309. 46811
/note="assembly_fragment"
46912. 192178
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clone_end:SP6
vector_side:left"
7750. .9020
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                   34048 CCCIGIAICTITIAACCTCCTIGITIAAGTTIGICTCTTCCAGAATCGAAGCTGTAAAACTA 34107
                                                                                                                                                                                                                                                                                                                                                      34108 caaaircericircaaardaagccccadargcadiccardacraadarcracdcdcddaccc 34167
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Kann, L.,
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1 (bases 1 to 192178)
1 shran, B. Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-1L20
                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGGACCGGCCTGCTAGCCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTTCCTGTTGAGAGGGGGGACTGAGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCGACCAATCAGAGGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 ACDAAAATGCTAATDAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 AGAGCACAGGGGGGGGGCATAGGATATAAACCCAGGCATTCGAGCCGGCAACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541 CAACCCCCTTTGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCACTCT
                                                                                                                                                                                                                                                                                        CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
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                                                                                                                                              1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAACTAAAACTA
                                                                     1; Gaps
                                                                     Indels
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                              Pred. No. 1.2e-161;
0; Mismatches 47;
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HTG; HTGS PHASE1; HTGS_DRAFT.
Homo sapiens (human)
Homo sapiens
                                      92.48;
                                                                            Conservative
                                          Local Similarity
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                                                                            Matches 587;
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SOURCE
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15179 chgshcrhactresarrcccrhactcchanaharrccrhactrangccrhactresanggrad 15238
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                                                                                          : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGAC-TAAGATCCACCGTGGACC 119
                                                                     Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                      end.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 TCATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGACTGAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA
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                                                                                                                                                                                                                                                                                                                      the SP6
                                      Direct Submission
Submitted (30-APR-2001) Genoscope - Centre National de Seq
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscop
- Web : www.genoscope.cns.fr)
On May 2, 2001 this sequence version replaced gi:13449984.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percentage of bases with a quality value >= 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 547.6; DB 9;
Pred. No. 1.5e-161;
0; Mismatches 39;
                                                                                                                                                                                                                                             Web site: http://www.genoscope.cns.fr/
Contact: SegRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
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/db xref="taxon:9606"
/chromosome="14"
/clone="R-784H12"
/clone="R-784H12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .192899
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Range : bases
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llarity 93.4%;
Conservative
(bases 1 to 192899)
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267
2595
4214
9526
27497
66134
82633
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hes 594;
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1 (bases 1 to 19289)

Heilig, R., Petir, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P., Brottlar, P., Cattolico, L., Barbe, V., Pelletier, E., Artiguenave, F., Levy, M., Eckenberg, R., Bruls, T., deBerardinis, V., Cruaud, C., Sequencing of the human chromosome 14

Uppublished
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Pred. No. 1.5e-161;
0; Mismatches 39;
                                                                                                                                 86.2%; Score 547.6;
llarity 93.4%; Pred. No. 1.5e
Conservative 0; Mismatches
       /note="assembly_fragment
clone_end:T7
vector_side:right"
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Submitted (09-MAY-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
5 (bases 1 to 172281)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                             ACO68492 172281 bp DNA linear PRI 29-OCT-2002
Homo sapiens BAC clone RP11-809C23 from 2, complete sequence.
ACO68492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (02-MAY-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                 15357 GAGAGCACAGCAGGAGGGCCAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACG
                                                                                                                                GAGAGCACAGGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACG
                                                                                                                                                                                                       GCAACCCCCTTTGGGTCCCCTCCCTTTGTATGGCCGCTCTGTTTTCACTCTATTTCACTC
                                                         CACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCT
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The sequence of Homo sapiens BAC clone RP11-809C23
Unpublished (2001)
3 (bases 1 to 172281)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                     15477 TATTAAATCTTGCAACTTCAAAAAAGAAAAAGATA 15512
                                                                                                                                                                                                                                                                                Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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Sulston, J.E. and Waterston, R.
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4 (bases 1 to 172281)
Waterston, R.
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6 (bases 1 to 172281)
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Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                  This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8 The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of RP11-809C23;
actual end is at base position 172281 of RP11-809C23.
Location/Qualifiers
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'rpt_family="MBR1_type"
124. .6274
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'rpt_family="MER1_type"
872. .3997
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/db xref="taxon:9606"
/chromosome="2"
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/rpt_family="MIR"
7990. .8112
/rpt_family="L2"
8188. .854^^
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161. _1218
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/rpt_family="ERVL"
3088. .3176
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/rpt_family="MIR"
4265. .447
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/rpt_family="L2"
____r="mBR2"
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1245. .1302
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1313. .1407
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repeat_region repeat_region

Center project name: H_NH0809C23

120

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Gaps

2;

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169418 bp DNA linear PRI 31-MAY-2002
Homo sapiens chromosome 3 clone RP11-66G8, complete sequence.
AC104163 AC073868
AC104163.2 GI:21281541
                                                                                                                                                                                                                                                                                              CIGGACCGGCCTAGCCCATGCICCGATGTTAATGACATTGAAGGCACCCCTCCCGAG 180
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2 (bases I to 169418)
2 (bases I to 169418)
3 birect Submission.
                                                                                                                                     17503 cccretarcrrraaccrccrretraagrrrercrcrccagaarcgaagcreraaacra 17562
                                                                                                                                                                                                                                                                                                                                   CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTTCCTGTTGAGAGGGGGGACTGAGAGAC 300
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 169418)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
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                                                                                                                                                                 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACGTGGACCC
                                                                                                            1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA
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                                                                                  Indels
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                                                      86.2%; Score 547.4; DB 9;
larity 92.4%; Pred. No. 1.7e-161;
Conservative 0; Mismatches 46;
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Submitted (05-DEC-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA Samphimmachak, C., Dison, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Samphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C. and Haugen, E.D. Direct Submission Submitted (31-MAY-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA On May 31, 2002 this sequence version replaced gi:17352427. Center: University of Washington Genome Center Center Code: UNGC Whe biter http://www.genome.washington.edu	Drafting Center: Wugger awaining content Drafting Center: WUGGE Project Information Center project name: chr-3 Center project name: RP11-6GB (bc0186) Summary Statistics Sequencing vector: unknown; 62% of reads	Sequencing vector: plasmid; LOWS 124; 348 for reads Chemistry: Dye-terminator E17: 668 of reads Chemistry: Dye-terminator Big Dye; 34% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 169322 bases at least Q40 Consensus quality: 169405 bases at least Q20 Consensus quality: 169418 bases at least Q20 Consensus quality: 169418, sum-of-contigs Consensus Quality: 109418, sum-of-contigs	Overlapping Sequences: 7. RP11-420K5 (UWGC:bc0651) AC104444, 57330-bp overlap 3': RP11-420X3 (UWGC:bc0659) AC104188, 73864-bp overlap Sequence Quality Assessment with sequence quality be been annotated with sequence quality	estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.	This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.	parison of the experimentally ence-predicted fragments is gidgested sequence consists of accurately represent the ention a variable cutoff (approximene fingerprint and hence do are no significant remaining ental and predicted values. Unated by dashed lines.	SeqDerMap FngrPrnt SeqDerMap FngrPrnt 8696 8873 8104 8155 459 <800

QY 481 AGAGCACAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGCAACGG 540 Db	RESULT 35 AC10444 AC10444 AC104444 AC104444 ACTOSSION DEFINITION Homo sapiens chromosome 3 clone RP11-420K5, complete sequence. ACCESSION AC104444.2 GI:20198385 KEYWORDS HTG. SOURCE HOMO sapiens (human) ORGANISM Homo sapiens		Subi Box 3 Kau	TITLE Direct Submission JOURNAL Southle, WA 98195, USA COMMENT On Apr 19, 2002 this sequence version replaced gi:17488626. COMMENT On Apr 19, 2002 this sequence version replaced gi:17488626. COMMENT On Apr 19, 2002 this sequence version replaced gi:17488626. Conter: University of Washington Genome Center Center Code: UNIVEC	Who be steen http://www.getolumer.webling.com.com Contact: uwgchtgs@u wachington.edu	Chemistry: Dye-terminator Big Dye, 11% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 160810 bases at least Q40 Consensus quality: 161049 bases at least Q30 Consensus quality: 161054 bases at least Q20 Insert size: 161054; sum-of-contigs Quality coverage: 11.0x in Q20 bases; sum-of-contigs	Overlapping Sequences: 5.: RPI1-24IK18 (UWGC:bc0320) AC104850 3.: Mapping in progress 3.: Mapping in progress Sequence Quality Assessment: This entry has been annotated with sequence quality restimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
2875 2969 2916 3846 1234 508 <800 3026 898 829 819 6096 <800 10620 10469 2347 2060 127 <800 6430 11089 2850 2916 3497	1112	4514 1105 2318 2318	5444 5340 6649 6736 7135 7167	Ouery Match Best Local Similarity 92.6%; Fred. No. 2e-16; Matches 587; Conservative 0; Mismatches 43; Indels 4; Gaps 1; Qy CCTGTANTTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCGAAAACTA 60 Dh 16015; CCCTGTAACTTCTTTAATCTTAATTTTTTTTTTTTTTTT		AGCGGT AGTGGT AGTGGT	Db 160275 CATCGGCCAACTCGCAACAGACTTTCCTGTTGAGAGGGGGGATTGAGAGT 160216 Qy 301 AGAACTAGCTGGATTTCCTAGGCCAACGAGAACCCTAAGCTTGGGATGTTTTGTGAGAGTGTT 360 L60215 AGACTAGCTGGATTTCCTAGGCTGACTTAGATCCCTAAGCCTGGAAGGTGACT 360 Qy 361 GCATCCACCTCTAAACATGCGGCTGCAACTTAGCTCACCCGACCAATCAGGAGGTC 420 L60155 ACATCCACCTTTAAACATGCGGCTTGCAACTTAGCTCACCCGACCAATCAGAGGGTC 160100 Qy 421 ACTAAAATGCTAATTAGGCAAAATAGGTAAAGAAAAAGAGCAATCATTGCTG 480 L60099 ACTAAAAATGCTAATTAGGCAAAAAAAAGGGGGTAAAGAAATAGCCAATCATTGCTG 160040

× 800	2	1862	3400	899	6176	5884	1282	1282	6692	3622	8947	4692	5884	<800	899	1587	4986	5884	1862	1110	<800															••	Gaps
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Direct Submission
Submitted (26-ARR-2001) Genoscope - Centre National de Sequencage :
BP 191006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
BP 191 91006 WWW. genoscope.cns.fr
On Apr 2, 2001 this sequence version replaced gi:13016608.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNSO6C7Q 169234 bp DNA linear PRI 28-APR-2001
Human chromosome 14 DNA sequence BAC R-21A20 of library RPCI-11
AL390799
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

(Dasea 1 to 1692a)

Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,

Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F.,

Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C.,

Gyapay,G., Saurin,W. and Weissenbach,J.

Sequencing of the human chromosome 14

Mubublished
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CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTAAAACTA
            CAAATTGITCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACGGTGGACCC
                                                             GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
       AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGAAGGTGACT
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                                                                  CTGGACCGGCCTGCTAGCCCCATGCTCCGATGACATTGAAGGCACCCTCCCGAG
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Pred. No. 1.7e-161;
0; Mismatches 37;
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/organisma"Homo sapiens"
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Embryogenesis associated proteins
Patent: WO 0248362-A 4 20-JUN-2002;
Incyte Genomics, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4 from Patent W00248362.
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Retrooviral nucleic material and nucleotide fragments, in particular, associated with multiple sclerosis and/or rheumatoid matchitis, for diagnostic, prophylactic and therapeutic uses Patent if 2002509437-A 9 26-MAR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                BD136199 1329 bp DNA linear PAT 18-SEP-20 Retroviral nucleic material and nucleotide fragments, in particular, associated with multiple sclerosis and/or rheumatoid arthritis, for diagnostic, prophylactic and therapeutic uses.
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07-UUL-1997 FR 97/08816
GLAUCIA PARAHNOS BACCALA FLORENCE KOMURIAN PRADEL, FREDERIC
                                                                                                             12531 CACTAAATGCTAATTAGGCAAAAACAGGAGGTAAAGAAATAGCCAATCATTTATTGCCT
                                                                                                                                                                         12589 recarccaccirraaacaceeeecrrecaacrivacricacaccaaccaarc--agagcr
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                                                                                                                                                  GAGAGCACAGCGGGAGGGACAAGGATCGGGATATAAACCCCAGGCATTCGAGCCGGCAACG
                                                                              CACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAAATCATTGCCT
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CC associated with multiple sclerosis and/or rheumatoid arthritis,
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                                                                                                                        Assembly program: Phrap; version 2.0
Quality coverage: 8.21x in Q20 bases; sum-of-contigs
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Genoscope / Centre National de Sequencage
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Location/Qualifiers
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larity 93.2%; Pred. No. 4.8e-161;
Conservative 0; Mismatches 40;
                                                                                       The following BAC sequence is oriented
                                  Web site: http://www.genoscope.cns.fr/
Contact: SegRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="matching EMBL: Z52518
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                                                                                                          .---- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/chromosome="14"
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136833. .137011
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Range : bases
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dbSTS:STS28504
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1 (bases 1 to 1329)
Ott.C. and Bedin,F.
RETROVIRL NOCLEIC MATERIAL AND NUCLEOTIDE FRAGMENTS, IN PARTICULAR
RETROVIRL NUCLEIC MATERIAL AND NUCLEOTIDE FRAGMENTS, IN PARTICULAR
ASSOCIATED WITH MULTIPLE SCLEROSIS AND/OR RHEUMATOID ARTHRITIS, FOR
DIAGNOSTIC, PROPHYLACTIC AND THERAPEUTIC USES
PATENT: WO 9902666-A 12 21-JAN-1999;
BIO MERIEUX (FR); OTT CATHERINE (FR)
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AGAGCACAGCGGGAGGGACAAGGATCGGGATATAAACCCCAGGCATTCGAGCCGGCAACGG
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                                   CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACGTGGACCC
                                                          CAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAAAATCTACCGTGGACCC
                                                                                 CTGGACCGGCCTGCTAGCCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
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Pred. No. 4.3e-161;
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Best Local Similarity 92.4%;
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Sequence 108 from patent US 6582703.
AR344389.1 GI:33740310
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/mol_type="mRNA"
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Best Local Similarity 92.4%;
Matches 572; Conservative
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RESULT 1
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Adb84397 MSRV-1 as
Aaa63826 Nucleotid
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AAX25661 AAA59211 AAH20069 AAD24195	ABL61744 AAX25665 AAAS9215 ABN97978 L ACN44334 ABN97929	ACN4458 AAI4608 AAA56337 AAI35980 ABA45822 ABA25978 AAK30018 AAK304516 ABS29670	AA104422 ABS04589 AD067414 AAX2563 AAA59213 ABA08902
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ALIGNMENTS

AAV43215 standard; cDNA; 635 BP

AAV43215;

New nucleic acid from retroviruses - useful for diagnosis, prevention and treatment of, e.g. multiple sclerosis. Multiple sclerosis associated retrovirus; MSRV; MS; pol gene; gag gene; env gene; rheumatoid arthritis-associated virus; ss. /*tag= a /product= "Encodes protein AAW71067" Multiple sclerosis associated retrovirus fragment 4. Perron H, Beseme F, Bedin F, Paranhos-Baccala Komurian-Pradel F, Jolivet-Reynaud C, Mandrand Multiple sclerosis associated retrovirus Disclosure; Page 183; 286pp; English. Location/Qualifiers 96US-00756429. 97WO-IB001482. (first entry) WPI; 1998-322732/28. P-PSDB; AAW71067. (INMR) BIO MERIEUX WO9823755-A1 26-NOV-1997; 29-DEC-1998 26-NOV-1996; 04-JUN-1998.

The present sequence represents a multiple sclerosis (MS) associated retrovirus (MSRV) genomic fragment used in the method of the invention.

AAF55630 AAX25660 AAA59210

ADQ94981

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CAACCCCTTTGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCACTCT
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The invention provides complete or partial genomic sequences of the MSRV-1 pol gene, gag gene and env gene, and polypeptides encoded by these genes. The invention also provides antibodies raised against the polypeptides. The genomic sequences, polypeptides and antibodies also claimed useful for diagnosing infection by MS and rheumatoid arthritisassociated viruses, and also for prevention and treatment of infection with these viruses
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                                                                                                                                                                     CTGGACCGGCCTGCTAGCCCCATGCTCGATGATGACATTGAAGGCCACCCTCCCGAG
                                                                                                         Gaps
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                                                                                       Length 635;
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This sequence represents clone CL6-3' from a novel multiple sclerosis related virus type 1 (MSRV1). The sequence can be used in diagnostic, prophylactic or therapeutic compositions to inhibit expression of a multiple sclerosis related virus and/or virus associated with rheumatoid polyarthritis. (Updated on 27-ANG-2003 to correct OS field.) (Updated on 17-OCT-2003 to standardise OS field)
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Nucleic acid sequences of retrovirus called MSRV-1 - associated with
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                                                                                                                                                                                                                                                                                  Sequence 635 BP; 188 A; 170 C; 136 G; 141 T; 0 U; 0 Other;
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ilarity 100.0%; Pred. No. 1e-186;
Conservative 0; Mismatchem n.
                             multiple sclerosis or rheumatoid polyarthritis
                                                                            Page 36-37; 83pp; French
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New isolated or purified nucleic acid associated with multiple sclerosis and/or rheumatoid arthritis, useful for detecting a virus associated with multiple sclerosis or rheumatoid arthritis in a biological sample.
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241 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGGACTGAGAGAC 300
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В В
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Jolivet-Reynaud C, Mandrand
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KOMURIAN-PRADEL F.
JOLIVET-REYNAUD C.
MANDRAND B.
GARSON J A.
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Komurian-Pradel F, J
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BESEME F.
BEDIN F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid which comprises the gene of a retrovirus associated with multiple sclerosis or rheumatoid arthritis. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating multiple sclerosis and/or rheumatoid arthritis. The present sequence is used in the exemplification of the invention.
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Mismatches 0
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Best Local Similarity 100.0%;
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97US-00979847.
                                                                                                                   standard; cDNA;
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multiple sclerosis-associated virus (MSRV)-1. The nucleic acids comprise pol, gag or reverse transcriptase genes (or their fragments) encoding the proteins or defined beptides (including immunodominant peptides, antiganic peptides or conserved motife). Also included are a process for detecting a virus associated with multiple sclerosis or rheumatoid arthritis in a biological sample, a nucleic acid probe for the detection of a virus associated with multiple sclerosis or rheumatoid arthritis, a primer for the amplification by polymerisation of a nucleic acid of a virus associated with multiple sclerosis or rheumatoid arthritis, a primer for the amplification by polymerisation of a nucleic acid of a virus material associated with multiple sclerosis or rheumatoid arthritis, a proteolytic, reverse transcriptase or ribonuclease H activity from MSRV, and an antibody directed against the MSRV-1 virus obtained by immunologically reacting the MTRV-1 virus obtained by immunologically reacting of the antigenic polypeptide defined above. The nucleic acids are useful for detecting a biological sample a virus associated with multiple sclerosis or rheumatoid arthritis. The present sequence is a claimed MSRV-search sequence of or exposure to a virus associated with multiple sclerosis or rheumatoid arthritis. The present sequence is a claimed MSRV-search sequence whose identity cannot be
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                                                                                                                                                                                                                                                                                                                                                                                                           accurately determined. Note: The SEQ ID numbers for the sequences as displayed in the main body of the patent do not match the SEQ ID number in the sequence listing. Consequently those sequences mentioned in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGGCTN
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Pred. No. 6.4e-184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide fragment of LTR-RUS region from Multiple Sclerosis retrovirus (MSRV) used to detect the presence of MSRV-1 retrovirus in a biological
                                                                                                                          MSRV-1; pol region; long terminal repeat; LTR; RU5 region; retrovirus;
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                                                                                                     Nucleotide sequence of the MSRV-1 3' env and LTR regions.
                                                                                                                                                                                    Location/Qualifiers
1. .1629
/*tag= a
/note= "Contains one termination codon"
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Best Local Similarity 98.3%;
Matches 624; Conservative
                      AAA63826 standard; DNA; 2030
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04-DEC-2000
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                                                                                                                                                                                                                                                                                                               TATA_signal
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RESULT 5
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CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA 60

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endometriosis, endometrial or ovarian tumour; autoimmune/inflammatory disorder such as acquired immune deficiency syndrome (AIDS), allergies, contact defamatitis; disorders of the placenta such as preclampsia, abruptic placente etc. Sequences of the invention are also useful for analysing a proteome of a tissue or a cell type. EMBRY proteins are useful as immunospens for preparing antibodies. Polynucleotides of the invention are useful for creating knockin humanised animals or transgenic animals to model human diseases. They are also used in gene therapy. The
                                                                                                                                                                                                                                                New polypeptides of human embryogenesis associated proteins for screening modulators useful for treating or preventing disorders e.g. endometriosis, infertility, allergy, preeclampsia.
                                                                                                                                                                                                                                                                                                                                                               invention relates to human embryogenesis associated proteins (EMBRY)
                                                                                                                                                                                                                                                                                                                                                                          and nucleic acid molecules encoding such proteins. EMBRY sequences are useful for screening modulators useful for treating or preventing disorders associated with abnormal expression of EMBRY. The disorders treated include reproductive disorders such as infertility.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence is human EMBRY-2 cDNA
                                                                                                                                                                                                                                                                                                                            Claim 59; Page 96-97; 97pp; English
                                                   14-NOV-2001; 2001WO-US043956
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llarity 93.8%;
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Best Local Similarity
Matches 579; Conserv
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                 20-JUN-2002
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CTGGACCGGCCTGCTAGCCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
                                                                                                                                                                                                                        GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGGGGGAAGCAGTTAGAGCGG
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                                                                                                                                                                                                                                                                                              AGGACTAGCTGGATTTCCTAGGCCAACGAATCCCTAAGCTTAGCTGGGAAGGTGACT
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                                                                                                                                                                                                   GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              embryogenesis associated protein; AIDS; reproductive disorder;
                                                       CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag= c
product= "Mature EMBRY-2 protein"
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Pred. No. 1.5e-158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
(revised)
(first entry)
  92.48;
  Best Local Similarity 92.4
Matches 572; Conservative
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27-AUG-2003
08-JUN-1999
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                    nucleic acid from retroviruses - useful for diagnosis, prevention and
                                                                                                                                                                                                                                                                                                                                                                         codon)
/transl_except= (pos:137-139, appears to code for a stop codon)
                                                                                                                                                                                                                                                                                                                                                              a stop
                                                                                                                                                                                                                                             Liple sclerosis associated retrovirus; MSRV; MS; pol gene; gag gene; gene; rheumatoid arthritis-associated virus; ss.
                                                                                                                                                                                                                                                                                              Location/Qualifiers
2. .490
/*tag= a
/product= "Encodes protein AAW71069"
/trans_except= (pos:77-79, appears to code for a stop
      AGAGCACAGCGGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
                                                                                                                                                                                                                                                                                                                                                            (pos:125-127, appears to code for
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Jolivet-Reynaud C, Mandrand
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                                                                                                                                                                                                                                                                              Multiple sclerosis associated retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment of, e.g. multiple sclerosis.
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                                                                                          601 ATTAAATCTTGCAACTG
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Komurian-Pradel F,
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Length 1329;

Score 545; DB 2;

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Query Match

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9
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rheumatoid polyarthritis; ss.
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                                                                                                                                                                                                  GCATCCACCTCTAAACATGGGGGTTGCAACTTAGCTCACACCGACCAATCAGAGAGGTC
                  cccretaricricaacriccristraagrirgicricriccagaarrgaaggraaaggra
                                   CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
                                               GAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGGAAGCAGTTAGAGCGGT
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New isolated nucleic acid and their fragments having the pol gene of a retrovitus, useful for diagnosing, preventing and/or treating multiple sclerosis and/or rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid which comprises the gene of a retrovirus associated with multiple sclerosis or rheumatoid arthritis. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating multiple sclerosis and/or rheumatoid arthritis. The present sequence is used in the exemplification of the invention.
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                                                                                                                         gene; retrovirus; multiple sclerosis; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1329 BP; 346 A; 352 C; 288 G; 340 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Bedin F, Paranhos-Baccala
Jolivet-Reynaud C, Mandrand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 545; DB 12;
Pred. No. 1.5e-158;
0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 108; 193pp; English
                                                                                                                                                                                    Multiple sclerosis associated retrovirus
                                                                                                                                                                                                                                                                                                                                                         03-APR-2002; 2002US-00114104
                                                                                                                                                                                                                                                                                                                                                                                                             96US-00756429
97US-00979847
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Best Local Similarity 92.4%;
Matches 572; Conservative
                       entry)
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                                                                           MSRV associated cDNA
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Komurian-Pradel F,
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                                                                                                                                                                                                                                                                        This sequence represents clone 5M6 from a novel multiple sclerosis related virus type 1 (MSRV1). The sequence can be used in diagnostic, prophylactic or therapeutic compositions to inhibit expression of a multiple sclerosis related virus and/or virus associated with rheumatoid polyarthritis. (Updated on 27-ANG-2003 to correct OS field.) (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1329 BP; 346 A; 352 C; 288 G; 340 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                     Nucleic acid sequences of retrovirus called MSRV-1 multiple sclerosis or rheumatoid polyarthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 545; DB 2; I
Pred. No. 1.5e-158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                         Claim 1; Page 39-40; 83pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
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nilarity 92.4%;
Conservative 0
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                                                          WPI; 1999-098275/09.
P-PSDB; AAW99554.
     (INMR ) BIO MERIEUX
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Best Local Similarity
Matches 572; Conserv
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                                                                                                                                                             19811 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGCACTGAGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
                                                                                                                                                                                                     CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGGACTGAGAGAC
                                                                                                                                                                                                                                                                   AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCCTAAGCCTAGCTGGAAGGTGACT
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                                                                                                                                       GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGGAAGCAGTTAGAGCGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human dithp growth/development-associated protein-encoding cDNA
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17-MAY-2001; 2001US-0291829P.
17-MAY-2001; 2001US-0291849P.
19-JUN-2001; 2001US-0299428P.
20-JUN-2001; 2001US-0299776P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-MAR-2001; 2001US-0279619P.
29-MAR-2001; 2001US-0280067P.
29-MAR-2001; 2001US-0280068P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUN-2003
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               61
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ACC46747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening drug candidates; (ii) for screening of bioactive agent capable of bioactive agent capable of modulating the activity of CAP; (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vi) for tagnosing carcinoma; (vii) for neutralizing the effect of CAP; (vi) for traating carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma are appropriately to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding capable of this patent is an equivalent to basic patent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19571 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATTGAAACTGTAAAACTA 19630
                                                                                                              900
                                                                                                                                            856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAACTGTAAAACTA
                                                                      CAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTTCACTCTATTTCACTCT
                                              AGAGCACAGGGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
                                                                                                            CAACCCCCTTTGGGTCCCCTTTCTTTGGGCGCTCTGTTTTCACTCTATTTCACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21646 BP; 5145 A; 5617 C; 5218 G; 5646 T; 0 U; 20 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 21646;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Cytostatic; carcinoma; lymphoma; cancer; human; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.6%; Score 543.4; DB 1:
94.8%; Pred. No. 1.8e-157
tive 0; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 910; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                      Human genomic sequence hCG1748307
                                                                                                                                                                             601 ATTAAATCTTGCAACTGAA 619
                                                                                                                                                                                                ATTAAATCATGCAACTGCA 875
                                                                                                                                                                                                                                                                                          ACN44454 standard; DNA; 21646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003; 2003WO-US006235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002; 2002US-00087192
                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-328604/31.
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nes 562; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                           857
                                                                                                                                                                                                                                                                                                                           ACN44454;
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                                                  481
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Matches
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ACN44454
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1163 593

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1051 AGAGCACAGCAGGGAGGGACAAGGATACGGGATATAAACCCGGGCATTCAAGCCGGCAATGG 1110
                                                                                                                                                                                                                                                                          The invention relates to an isolated or purified nucleic acid from a virus associated with multiple sclerosis and/or rheumatoid arthritis, unltiple sclerosis associated virus (MSRV)-1. The nucleic acids comprise pol, gag or reverse transcriptase genes (or their fragments) encoding the proteins or defined peptides (including immunodominant peptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated or purified nucleic acid associated with multiple sclerosis and/or rheumatoid arthritis, useful for detecting a virus associated with multiple sclerosis or rheumatoid arthritis in a biological sample.
                                                                                                                                                      GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
                                                                                                                                                                                  421 ACTABAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
                                                                     AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
                                                                                                                                                                                                                                                                                                                                   AGAGCACAGCGGGAGGACAAGGATCGGGATATAAACCCCAGGCATTCGAGCCGGCAACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garson JA,
                                                                                                                                                                                                                                                                                                                                                                                                                         ds; multiple sclerosis; rheumatoid arthritis; gag; pol; reverse transcriptase; ribonuclease H.
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Jolivet-Reynaud C, Mandrand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSRV-1 associated DNA sequence #21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 31; Page 80; 193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADB84403 standard; DNA; 1329 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KOMURIAN-PRADEL F.
JOLIVET-REYNAUD C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-512253/48
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GARSON J A.
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BESEME F.
BEDIN F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TUKE P W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2003039664-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified;.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-DEC-2003
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(MAND/)
(GARS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TUKE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PARA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KOMU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BESE/)
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ADB84403
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C polymucleotides designated dithp (ACC46080-ACC46749) and to their encoded
proteins (DITHP; ABR4136-ABR41812). The invention also relates to
polymucleotide sequences at least 90% identical to the dithp CDNA
c proteins (DITHP; ABR4136-ABR41812). The invention also relates to
c polymucleotide sequences at least 90% identical to the dithp CDNA
c sequences of the invention; recombinant vectors, host cells and
c recombinant production of DITHP proteins; antibodies specific for DITHP
c recombinant production of DITHP proteins; antibodies specific for DITHP
c proteins microarrays comprising dithp nucleic acid sequences; methods of
detecting dithp nucleotide and protein sequences; methods of
c corpounds which specifically bind a DITHP proteins and methods of
c assessing the toxicity of test compounds using a dithp hybridisation
c probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
diagnosis of a wide variety of conditions including cancer and other cell
c proliferative disorders; autoimmune or inflammatory disorders; bacterial,
viral, fungal or parasitic infections; hormonal disorders; metabolic
c disorders; neurological disorders; gastrointessinal disorders; transport
c disorders; neurological disorders; gastrointessinal disorders; transport
c disorders; and connective tissue disorders. They may also be used to
screen for modulators of protein activity or gene expression. DITHP
c proteins can additionally be used in analysis of the proteome of a tissue
c or cell type and to induce antibodies. The dithp nucleic acids are
c additionally useful in somatic or germine gene therapy of the disorders
mentioned above, as a source of antisense sequences, as a source of
probes and primers, in genotyping and identification of individuals, in
the generation of transgenic animal models of human disease or knock in
the generation of transgenic animal models of human disease or knock in
the generation of the protein active set
c for this patent di
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                                                                                                                                                                                                                                                                                              Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polypeptide encoded by human diagnostic and therapeutic polynuclectide, and to induce antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTA
                                                                                                                        n DA, Kleefeld Y, Gerstin EH;
n AJ, Panzer SR, Harris B;
Urashka ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                   Chinn J;
Amshey SR;
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Pred. No. 5.6e-157;
0; Mismatches 33; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2046 BP; 587 A; 494 C; 391 G; 566 T; 0 U; 8 Other;
                                                                                                   Gietzen D,
O, Yap PE,
                                                                                                 Daffo A, Jones AL, Tran AB, Dahl CR, Giet Dufour GE, Hillman JL, Yu JY, Tuason O, Y Daughtery SC, Dam TC, Liu TF, Nguyen DA, Paca GH, David MH, Lewis SA, Chen AJ, Flores V, Marwaha R, Lo A, Lan RY, Urashb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; SEQ ID NO 668; 591pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.1%;
                20-JUN-2001; 2001US-0300001P.
                                                            (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                            P-PSDB; ABR41810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 560;
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AAX77526 standard; cDNA; 2946

entry)

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10-AUG-1999

AAX77526;

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detecting a virus associated with multiple sclerosis or rheumatoid arthritis in a biological sample, a nucleic acid probe for the detection of a virus associated with multiple sclerosis or rheumatoid arthritis, a primer for the amplification by polymerisation of a nucleic acid of a virus associated with multiple sclerosis or rheumatoid arthritis, a primer for the amplification by polymerisation of a nucleic acid of a virus associated with multiple sclerosis or rheumatoid arthritis, a polypeptide exhibiting an inhibitory activity on the proteolytic, reverse transcriptase or ribonuclease H activity from MSRV, and an antibody directed against the MSRV-1 virus obtained by immunogenic agent consisting of the antigenic polypeptide defined above. The multiple sclerosis or rheumatoid arthritis, or for detecting in a biological sample, the presence of or exposure to a virus associated with multiple sclerosis or rheumatoid arthritis. The present sequence is a claimed MSRV-associated sequence whose identity cannot be accurately determined. Note: The SEQ ID numbers for the sequences as a displayed in the main body of the patent do not match the SEQ ID numbers in the sequence listing. Consequencely those sequences mentioned in the claims may not be the sequences the authors intended to claim.
                8888888888888888888888888
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Sequence 1329 BP; 339 A; 346 C; 282 G; 332 T; 0 U; 30 Other;

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Score 535; DB 9; Length 1329;
Pred. No. 1.9e-155;
0; Mismatches 57; Indels
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This invention describes novel human secreted proteins encoded by polynucleotides isolated from human adult testes, adult brain, adult blood or adult placenta, or murine adult bone marrow or thymus cDNA blood or adult placenta or murine adult bone marrow or thymus cDNA activities which would make them invention are predicted to have biological activities which would make them wuitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haemostatic and thrombolytic activity, rhemotactic/emeokinnetic activity, haemostatic activity, and thrombolytic activity, receptor/ligand activity, and tumour cativity, adharin/tumour invasion suppressor activity, and tumour continity. The polynucleotides are also stated to be useful for
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                                                                                                                                  Secreted protein; testes; brain; blood; placenta; human; murine; thymus; bone marrow; treatment; prevention; nutrition; cytokine; immune; vaccine; cell proliferation; cell differentiation; suppressor; tumour inhibition; haematopoiesis regulator; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; receptor; ligand; anti-inflammatory; tumour; cadherin; tumour invasion suppressor; gene therapy; tissue growth; ss.
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                                                                                                      Human secreted protein AJ172_2 cDNA
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Merberg D, Treacy M;
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This is the human secreted protein AJ172 2 nucleotide sequence, obtained from a human adult testes cDNA library. The invention relates to secreted from a number proteins. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Detection of the levels of the proteins can be used for the diagnosis of e.g. pre-eclampsia, placencial pathology or cancer. Agents which modulate the expression or function of the proteins may be used for treating a neoplastic disease and inhibiting metastasis. Other suggested activities include nutritional activity (e.g. in feeds), cytokine and cativities include nutritional activity, immune stimulating (e.g. as vacines) or suppressing activity, haemactopiesis regulating activity, clissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemactory activity, cadherin/tumour creceptor/ligand activity, and tumour inhibition activity. The invasion suppressor activity, and tumour inhibition activity. The polynucleotide sequences are also stated to be useful for gene therapy
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Pred. No. 6.6e-155;
0; Mismatches 42; Indels 12;
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                                                                                                          2731 ACTAAAATGCTAATTAGGCAAAAACAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
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                                            GABARTCTCAGCTGCACAACCTCTACTACGCCCCAATTCAGCAGGAAGCAGTTAGAGCGGT
                                                                                      CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTTCCTGTTGAGAGGGGGACTGAGAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted protein; disease diagnosis; pre-eclampsia; cancer; placental pathology; metastasis inhibition; nutritional activity; immune stimulator; haematopoiesis regulator; tissue growth; tumour inhibitor; anti-inflammatory; clone AJ172_2; ATCC_98115; gene therapy; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΰ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 14; Page 107-108; 149pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lavallie ER,
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Mi S, Treacy M;
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Merberg D,
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WPI; 2003-657236/62.
P-PSDB; ADC38777.
                                                                      US2002193567-A1.
                                                               Homo sapiens.
                                                                                                                                                                         Jacobs K, M
Merberg D,
Kelleher K;
                                                                                           11-AUG-1995
05-APR-1996
                                                                                                     07-JUN-1996
17-JUN-1996
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26-JUL-1996
                                                                                                                               27-SEP-1996
27-SEP-1996
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30-OCT-1996
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10-APR-1997
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          18-DEC-2003
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   ADC38776;
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CAACCCCTTTGGGTCCCCTCCCTTGTATGGGAGCTCTGTTTTCATGCTATTTCACTCT 2910
coagulation disorders, inflammatory diseases (e.g. systemic inflammatory response syndrome (SIRS), ischaemia-reperfusion injury, Crohn's disease), anaphylaxis and hypersensitivity. Proteins are also useful for inducing tumour immunity, for inducing bone, cartilage, tendon, ligament and/or nerve growth or regeneration, for proliferating neural cells and for inhibiting tumour growth. Proteins are also useful as chemokine for mammalian cells (e.g., monocytes, fibroblasts, neutrophils), and also useful as inhibitors of receptor/ligand interactions. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ds; gene; serine/threonine protein kinase; inflammation; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2431 CTGGACCGGCCTGCTAGCCCACGATCTGATGTTAATGACATCAAAGGCCACCCTCCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1491 GAAATCTCAGCTGCACAACCTCTACTACGCCCCCAATTCAGCAGGAAGCAGTTAGAGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2611 AGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCTAAGCCTAGCTGGGAAGGTGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 CTGGACCGGCCTGCTAGCCCATGCTCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                   CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA
                                                                                                                                                                                                                                                                                                                    DB 10; Length 2946;
                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                     Sequence 2946 BP; 858 A; 801 C; 570 G; 717 T; 0 U; 0 Other;
                                                                                                                                                                                                                        sequence represents cDNA encoding a human secreted protein.
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Pred. No. 6.6e-155;
0; Mismatches 42;
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                                                                                                                                                                                                                                                                                                                       Query Match 84.1%;
Best Local Similarity 91.5%;
Matches 581; Conservative
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XX DT 16-O
DT 16-O
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                                                                                                                                                                                                         autolmmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; allorgic reaction; asthma; myeloid cell deficiency; pymphoid cell deficiency; osteoporosis; osteoarthritis; peripheral nervous system disease; peripheral neuropathy; Alzheimer's disease; Parkinson's disease; coagulation disorder; inflammatory disease; systemic inflammatory response syndrome; SIRS; ischaemia-reperfusion injury; Crohn's disease; anaphylaxis; hypersensitivity; regeneration; neural cell proliferation; fertility; tumour; chemokine; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proteins AZ3021 encoded by clone AZ3021 from human adult colon, and BD12716 encoded by clone BD12716 from human fetal kidney cDNA library, useful for treating e.g. multiple sclerosis and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Σ
                                                                                                                                                                                     severe combined immunodeficiency; SCID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collins-Racie LA, Evans C;
Spaulding V, Carlin-Duckett
                                                                                                                                           Human cDNA encoding a secreted protein #63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 134; 412pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lavallie ER,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-00514014.
96US-00653314.
96US-00659224.
96US-00664596.
96US-00666878.
96US-0070211.
96US-00711798.
96US-00721128.
96US-00721728.
96US-00721923.
96US-00738367.
96US-00738367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-APR-2002; 2002US-00114893
                                                                                                                                                                                        gene; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEMY ) GENETICS INST INC.
                                                                                              (first entry)
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300

2430

2382

9

Gaps

2490

240

180

2670

420

360

2730

2790

480

540

/*tag= bb /standard_name= "Single nucleotide polymorphism" on replace(31808,T) /*tag= hr	/standar /standar replace(/*tag= /standar replace(/*tag= be /standard name= "Single nucleotide polymorphism" on replace(3518,G)	~ M ·	/*tag= /standaz replace	``	replace(37050,G) /*tag= bi	. -	``	replace(37481,A) /*tag= bk	/standard name= "Single nucleotide polymorphism" on replace(37499,T)		replace(4017840179,GRA) /*tag= bm	/standar replace(/ ray= Di /standard name= "Single nucleotide polymorphism"	replace (44582, G) /*tag= bo	/Brandard names "Single incleoting replace (45615, A) /*than= hn	/scag= /standar	-	/ Schloat Chamber Single metalocal replace (47844,C) (************************************	/standar replace(replace(48072,A) /*tag= bt		/ reag= bu /standard name= "Single nucleotide polymorphism"	/*tag= bv	replace(53378, .53380, GG)	/standard name= "Single nucleotide polymorphism"		7.1ulliDel= 2 7.1ulliDel= 2 5.30483114 7.************************************		on replace(56233,G)
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? kinase; transgenic; chromosome 3; SNP;	ers .	1140,GGT) "Single nucleotide polymorphism"	replace(1399,G) /*tag= aj /standard_name= "Single nucleotide polymorphism"	1873,TG) "Single nucleotide polymorphism"	loa	3000323016 /*rad= a	"Serine/threonine protein kinase" 59				"Single nicleotide nolvmorphism"		"Single nucleotide polymorphism"	"Single nucleotide polymorphism"		"Single nucleotide polymorphism")	*tag= aq standard_name= "Single nucleotide polymorphism"	3	"Single nucleoride polymorphism")	*tag= as standard name= "Single nucleotide polymorphism"	.1240/,111) "Sinale musleotide polymorphism"		standard name= "Single nucleotide polymorphism" spandard	"Single nucleotide polymorphism"		"Single nucleotide polymorphism")	"Single nucleotide polymorphism"		"Single nucleotide polymorphism")	"Single nucleotide polymorphism"		"Single nucleotide polymorphism"
arteriosclerosis; psoriasis; SNF kinase; transgenic; single nucleotide polymorphism.	o sapiens.	iation		variation replace(18711 /*tag= ak /standard_name=	variation replace(18751877,TA) /*tag= al /arandard_name= "Single	CDS 323016 (*Face a /*Face a	1, t		l LO	/ rags c /number= 1 variation replace(3180.G)		variation replace (7590, A)	e ar		variation replace(9572,A) /*tag= ap	/standard_name= variation replace(11004,G)		variation replace(11379. /*tag= ar	ie i		variation replace(12486 /*tag= at /standard name=	variation replace (13904, G)	/ / Btandard name= variation replace (25444.		variation replace(26805,A) /*tag= aw	/standard_name≂ variation replace(28010,R)	/*tag= ax /standard_name= //standard_name=	Variation replace(2810/,r. /*tag= ay	/standard_name= variation replace(28178,R)	/*tag= az /standard_name=	variation replace(28356,T /*tag= ba	/standard_name=
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H (<pre>/*tag= ak /*tad=rd name= "Single nucleotide polymorphism (SNP)" replace(45615,A) /*teg= al</pre>	Single nucleotide polymorphism (SNP)	<pre>/standard_name= "Single nucleotide polymorphism (SNP)" replace(47844,C) /*tag= an /*randard name= "Single nucleotide polymorphism (SNP)"</pre>	"Single nucleotide polymorphism	"Single nucleotide polymorphism	<pre>replace(50802,T) /*tag= aq /standard name= "Single nucleotide polymorphism (SNP)"</pre>	replace(53305,A) /*tag= ar /standard name= "Single nucleotide polymorphism (SNP)"		.5 <u>3</u> 903 at .83114	au (56233,G) av	<pre>ard name= "Single nucleotide e(56453,C) aw</pre>	ard name= "Single nucleotide e(59300,T)	ar e (ordiname= "Single nucleotide polymorphism (SNP) s(63013,A) az	<pre>ard_name= "Single nucleotide polymorphism (SNP) e(63293,A) ba</pre>	ard_name= "Single nucleotide polymorphism (SNP) (64181,T)	/standard_name= "Single nucleotide polymorphism (SNP)" replace(64191,A) /*tan= hc1	indiname= "Single nucleotide polymorphism (SNP) e(68992,C)	ard name= "Single nucleotide polymorphism (SNP) 176 246,Y)	<pre>/standard_name= "Single nucleotide polymorphism (SNP)" replace(77368,G) /*tandard_name= "Single nucleotide polymorphism (SNP)" /*tandard_name= hf</pre>	e (ar e (/"tag= bn /standard_name= "Single nucleotide polymorphism (SNP)" replace(79474,G)
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The present sequence encodes a human endogenous retrovirus envelope protein. The specification describes a method for detecting expression of an envelope protein from a human endogenous retrovirus (HERV), in cells, of a tissue or culture. The method comprises detecting syncytia formation due to the fusogenic properties of the envelope protein. Envelope polypeptides and polymucleotides are used to produce therapeutic or prophylactic compositions, particularly for treatment of cancer, to correct defects in placental development (or other natural formation of other types of syncytia), and to promote adhesion of cells in grafts or cellular repair processes. Expression of sequences antisense to the polymucleotide are used to prevent formation of syncytia
                                                                                                                                                                                                                                                                     Detecting expression of human endogenous retrovirus envelope protein in cells of a tissue or culture, from its ability to induce syncytia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 532.2; DB 5; Length 2781;
Pred. No. 2e-154;
0; Mismatches 43; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2781 BP; 747 A; 770 C; 556 G; 708 T; 0 U; 0 Other;
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/product= "envelope protein"
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(INRM ) INST NAT SANTE & RECH MEDICALE.
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91.3%;
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Matches 580; Conservative
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/standard name= "Single nucleotide polymorphism (SNP)"
replace (7992,T)
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syncytia; cancer; cell adhesion; ss.
                                                                                          Length 326014;
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                                                                                            DB 12;
                                                                                          83.9%; Score 532.8; DB 12;
larity 90.5%; Pred. No. 1.3e-153;
Conservative 0; Mismatches 52;
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                  GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCGACCAATCAGAGGCTC
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CTGGACCGGCCTGCTAGCCCATGCTCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
                                                           GAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pol gene and 3' non coding sequences of HERV-W from human genome
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                                                                                                                                                                                                                                                                                                                                                                     Clone; human endogenous retrovirus; genome; autoimmune disease; multiple sclerosis; rheumatoid polyarthritis; insulin-dependent diabetes; disseminated lupus erythematosus; pregnancy; chromosomal marker; ss.
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                                       2685 CAACCCCCTTTGGGTCCCCTCTCTTGTATGGGAGCTCTGTTTTCATGCTATTTCATGCTTTT
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Pred. No. 1.3e-152;
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90.7%;
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polyarthritis; insulin-dependent diabetes;

disseminated lupus erythematosus; pregnancy; chromosomal marker; ss.

sclerosis, rheumatoid

multiple

endogenous retrovirus

Human

98WO-FR001442 97FR-00008815

06-JUL-1998; 21-JAN-1999

(INMR) BIO MERIEUX

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fragment, which is associated with an autoimmune disease, and is integrated into the human genome. The fragment is originally derived from a novel retrovirus, human endogenous retrovirus W (HERV-W). The HERV-W retrovirus is associated with autoimmune disease, failure of pregnancy or disorders of pregnancy. The nucleic acid fragment, or proteins derived from it, are useful for diagnosis of autoimmune disease (specifically multiple sclerosis) and for monitoring pregnancy. The nucleic acid fragments may also be used for in situ labelling of isolated chromosomes, while the transcription product can be used to study or monitor T cell
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Pred. No. 1.3e-152;
0; Mismatches 47;
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Pred. No. 2e-151;
); Mismatches 49;
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Clone; human endogenous retrovirus; genome; autoimmune disease;

Human endogenous retrovirus W clone cl.PH74

BP 2782

mRNA;

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standard; cDNA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2566 ACTADADATGCTAATTAGGCADAGACAGGAGGTADAGADAATAGCCAATCATTATTGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human endogenous retrovirus; HERV-W; HERV; chromosome 7; env protein; envelope protein; multiple sclerosis-related superantigen; vaccine; surface antigen; transmembrane; multiple sclerosis; neuroprotective; antisense-therapy; autoimmune disorder; ds.
                                  2266 CTGGACCGGCCTGCTAGCCCACGATCTGATGTTAATGACATCAAAGGACCCCTCCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
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241 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCGGACCAATCAGAGAGCTC
                                                                                                                                181 GAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
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(pos:792. .792.aa:Phe)

(pos:812. .795,aa:Thr)

(pos:812. .864,aa:Leu)

(pos:818. .820,aa:Ser)

(pos:865. .864,aa:Tyr)

(pos:1774. .1176,aa:Tyr)

(pos:1174. .1176,aa:Tyr)

(pos:1174. .1176,aa:Tyr)

(pos:1174. .1176,aa:Tyr)

(pos:1174. .1176,aa:Tyr)

(pos:1174. .1176,aa:Tyr)

(pos:1174. .1176,aa:Tyr)

(pos:2017. .2019,aa:Lys)

(pos:2017. .2019,aa:Lys)

(pos:20189. .2091,aa:Arg)
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                                             2685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Autoimmune disease; retrovirus; human endogenous retrovirus W; HERV-W; gag gene; pregnancy; multiple sclerosis; T cell proliferation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA
   2686 CAACCCCCTTTGGGTCCCCTCCCTTTGTATGGGAGCTCTGTTTTCATGCTATTTCACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                        CAACCCCCTTTGGGTCCCCTCCCTTGTATGGGCGCTCTGTTTTCACTCTATTTCACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5' non coding, 3' pol gene, and 3' non coding sequences of HERV-W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49; Indels 12;
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Pred. No. 2e-151;
0; Mismatches 49;
                                                                                                                                                                                                                                                                                     ATTAAATCTTGCAACTGAAAAAAAAAAAAAAAAAAAA 635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 46-47; 53pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВР
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90.4%;
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2386 GGTCGGCCAACTCCCCAACAGCACTTAGGTTTTCCTGTTGAGATGGGGGACTGAGAGAC 2445
                                                                                                                                                                                                                                                                             The invention relates to identifying compounds which are modulators of syncytin expression. The syncytin modulators are useful in diagnosis and treatment of preeclampsia and gestational trophoblast disorders (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying a compound for treating a subject with or at risk of developing preeclampsia, comprises determining whether the expression or activity of syncytin in the cell is modulated in the presence of a test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2686 CAACCCCCTTGGGTCCCCTTTGTATGGGAGCTCTGTTTTCATGCTATTTCACTCT
                                                                                              2446 AGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCTTAAGCCTAAGGTGGGAAGGTGACC
                                                                                                                                                                              481 AGAGCACACAGCGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
                                                                                                                                                                                                                                                                                                                                                                                           2626 AGAGCACAGCAGGAGGGACAATGATCGGGATATAAACCCAAGTTTTCGAGCCGGCAACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                            541 CAACCCCTTTGGGTCCCCTTCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCACTCT
                                                   AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGAAGGTGACT
                                                                                                                                               361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGGGCTC
                                                                                                                                                                                                                                                421 ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, syncytin, preeclampsia, gestational trophoblast disorder, choriocarcinoma, hydatiform mole, placental site tumour, abortion, envelope gene, human endogenous defective retrovirus; HERV-W, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            601 ATTAAATCTTGCAACTGAAAAAAAAAAAAAAAA 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 39-42; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/product= "Syncytin"
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930. .2546
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Keith JC, Mccoy JM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              condependent retrovirue (HERVB) the full length endogenous provirus which was been located on the long arm of human chromosome 7 (7021-21) has been designated HERV-W. The present invention describes proteins or peptides (Ed Signated HERV-W. The present invention describes proteins or peptides (I) having superantigen (594) activity comprising the ENV protein (ENV) of HERV-W, the surface protein (5U) and transmembrane (TM) sub-unite: (I) eave neuroprotective activity, and can be used in: vaccines; antisenserch therapy; and HERV-W SAG activity, and can be used in: vaccines; antisenserch disporders. (I) are also useful for identifying substances (and optionally recovering) capable of binding to a retroviral superantigen associated with MS, substances capable of blocking standardian of HERV-W retroviral superantigen. A protein or peptide derived from (I); modified to be used of Sag activity and being capable of generating an immune response conding (I) are useful as vaccines against MS. Substances against HERV-W retroviral SAG activity, capable of blocking transcription or translation of HERV-W retroviral sagerul in therapy. Nucleic acid molecules encoding (I) are useful as vaccines against MS. Substances capable of blocking SAG activity, capable of blocking transcription or translation of HERV-W retroviral superantigen for use in treating or translation of HERV-W retroviral superantigen for use in treating or translation of HERV-W retroviral superantigen for use in treating or preventing MS. Obtained using (I) are useful for the treatment and prevention of MS. (I) and nucleic acids encoding them are useful for specifically claimed envelope protein of HERV-W designated G specifically of HERV-W envelope protein of HERV-W designated G specifically of HERV-W envelope protein of HERV-W designated G specifically of HERV-W envelope protein of HERV-W designated G specifically designated G specifically designated G sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human retrovirus HERV-W ENV proteins/peptides having superantigen activity useful for diagnosing and treating multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.3%; Score 522.6; DB 5; Length 2782; 90.4%; Pred. No. 2e-151; ive 0; Mismatches 49; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2782 BP; 741 A; 768 C; 564 G; 709 T; 0 U; 0 Other;
                 /transl_except= (pos:2170. .2172,aa:Asn)
2380. .2782
/*tag= c
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Matches 574; Conservative
                                                                                                                                                                                                                                                                                                                   (UYGE-) UNIV GENEVE.
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30-MAY-2001; 2001WO-US010838
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             Homo sapiens.
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
gene; ds.
choriocarcinoma, hydatiform mole, placental site tumour and missed/
incomplete abortion). Syncytin is a human gene derived from the envelope
gene of human endogenous defective retrovirus, HERV-W. The present
invention is based partly on the discovery that syncytin expression is
dramatically reduced in preclampsia, and is also mis-localised to the
apical syncytiotrophoblast membrane. The present sequence is human
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                                                                                                                                                    CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTTCCAGAATCAAAACTA
                                                                                                                                Gaps
                                                                                                                                12;
                                                                                                         Length 2930;
                                                                                     Sequence 2930 BP; 842 A; 800 C; 571 G; 717 T; 0 U; 0 Other;
                                                                                                                                Indels
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                                                                                                                                 41;
                                                                                                           Score 517.4; DB 6;
Pred. No. 8.3e-150;
                                                                                                                                0; Mismatches
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                                                                                                         81.5%;
ilarity 91.4%;
Conservative
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                                                                                                         Query Match
Best Local Similarity
Matches 564; Conserv
                                                                 syncytin cDNA
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anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                                                                                                                       180
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                                                                                                                                                                                      Gaps
                                                                                                                                 Sequence 56093 BP; 16164 A; 12346 C; 10702 G; 16881 T; 0 U; 0 Other;
                                                                                                                                                          Length 56093;
                                                                                                                                                                                      12;
                                                                                                                                                                                        Indels
                                                                                                                                                             .2; DB 6;
8.3e-149;
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                                                                                                                                                                                                                    CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCT
                                                                                                                                                                                         0; Mismatches
                                                                                                                                                               Score 516.2;
Pred. No. 8.3
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                                                                                                                                                             ch 81.3%;
al Similarity 91.1%;
564; Conservative
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Best Local S
Matches 564
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                                                                                                                                                                                                                                                                                                        This sequence represents the complete sequence of the human endogenous retrovirus (HERV) W genome. The nucleic acids, their fragments or peptides encoded by them are markers of autoimmune disease (e.g. multiple sclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulin- dependent diabetes and related pathologies) and of abnormal or suscepstiblity to these conditions, or proximity markers for susceptiblility to these conditions, or proximity markers of genes
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                                                                                                                                                                                                                              New nucleic acid sequences from human endogenous retrovirus-W - expressed exclusively in placenta and useful in diagnosis and therapy of autoimmune disease, and abnormal or failed pregnancy.
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 88
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7582 BP; 2156 A; 1877 C; 1537 G; 1796 T; 2 U; 214 Other;
marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 7582;
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disseminated lupus erythematosus; pregnancy; chromosomal
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                                                                                                                                                                                Mallet
                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.5%; Score 511.4; DB 2;
89.5%; Pred. No. 9.8e-148;
iive 11; Mismatches 42;
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                                                                                                                                                                                 Mandrand
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                                                                                                                                  97FR-00008815
                                                                                                                                                                                    Bouton
                            retrovirus
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                                                                                                                                                          (INMR ) BIO MERIEUX
                               Human endogenous
                                                       WO9902696-A1
                                                                                                         06-JUL-1998;
                                                                                                                                  07-JUL-1997;
                                                                               21-JAN-1999
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The present sequence represents an endogenetic retrovirus, which is associated with an autoimmune disease, and is integrated into the human genome. The retrovirus is human endogenous retrovirus W (HERV-W). The HERV-W retrovirus is associated with autoimmune disease, failure of pregnancy or disorders of pregnancy. HERV-W nucleic acid fragments, or proteins derived from it, are useful for disgnosis of autoimmune disease (specifically multiple sclerosis) and for monitoring pregnancy. The nucleic acid fragments may also be used for in situ labelling of isolated chromosomes, while the transcription product can be used to study or
                                                                                                                                                                                                                                                                                                            120
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                                                                                                                                                              Sequence 7582 BP; 2156 A; 1876 C; 1538 G; 1796 T; 0 U; 216 Other;
                                                                                                                                                                                                                       12;
                                                                                                                                                                                           Length 7582;
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                                                                                                                                                                                                                       Indels
                                                                                                                                                                                           ; Score 511.4; DB 3;
; Pred. No. 9.8e-148;
11; Mismatches 42;
                                                                                                                                      monitor T cell proliferation in vitro
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Best Local Similarity 89.5<sup>3</sup>
Matches 552; Conservative
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                                       CAACCCCCTTTGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCACTCT
                                                                   CAACCCCCTTTGGGTCCCCTTCCTTTGTATGGGAGCTCTGTTTTCATGCTATTTCACTCT
                                                                                                                                                                                                                                                                                                                  Dimmune disease; retrovirus; human endogenous retrovirus W; gene; pregnancy; multiple sclerosis; T cell proliferation;
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/note= "ORF3 48 AA"
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note= "U3-R of 3' LTR'
                                                                                                                                                                                                                                                                                       retrovirus W (HERV-W)
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1. .120
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The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (1) for screening of bioactive agent capable of chinding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for a bioactive agent capable of modulating the activity of CAP; (iv) for unitibiting the activity of CAP; (vi) for treating carcinoma; (vii) for inhibiting the effect of CAP; (vii) for treating carcinoma; (vii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for (X) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for carcinoma the useful as DNA vaccines and the CAP are useful as Markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent capable of capable o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      591
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                                                                                                                                                                                                                                                                                                                                                                                                              33874 CTTCACTCTATTAAATATTGCAACTGCAAAAAAAAAATA 33912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytostatic; carcinoma; lymphoma; cancer; human; gene;
                                                                                                                                                                                                                                                                                                                                                                        592 TITCACICIATIAAAICITGCAACIGAAAAAAAAAAA 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 510.6; DB 11;
Pred. No. 7.7e-147;
0; Mismatches 49; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 730; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genomic sequence hCG32959
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Local Similarity 90.0%;
es 575; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002; 2002US-00087192.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to new nucleic acid sequences of human endogenouse retrovirus, HERV-7q, which is located on chromosome 7q.

Regulatory elements associated with HERV-7q may alter expression of other genes (even remote genes) on the same chromosome, inducing immunological and/or neurological changes (which may be pathological or protective) curative). HERV-7q peptides can be used to improve efficiency of the immune response, e.g. in immunotherapy. HERV-7q peptides and their coding sequences can be used in immunoquence or vaccinating compositions, for protection against autoimmune diseases, particularly multiple sclerosis. The peptides may also be used (by sequence comparison) to detect/identify endogenous retroviruses that are abnormally expressed in cancer, neuropathologies or other autoimmune diseases. The present sequence was used to illustrate the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 CTGGACCGGCCTGCTAGCCCATGCTCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
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Pred. No. 4.2e-147;
0; Mismatches 49;
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                                                                                                        Human endogenous retrovirus
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                                         multiple sclerosis;
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es 575; Conserv
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                                                  The present invention relates to new nucleic acid sequences of human endogenouse retrovirus, HERV-7q, which is located on chromosome 7q. Requiatory elements associated with HERV-7q may alter expression of other genes (even remote genes) on the same chromosome, inducing immunological and/or neurological changes (which may be pathological or protective/curative). HERV-7q peptides can be used to improve efficiency of the immunotherapy. HERV-7q peptides and their coding sequences can be used in immunogenic or vaccinating compositions, for protection against autoimmune diseases, particularly multiple sclerosis. The peptides may also be used (by sequence comparison) to detect/identify endogenous retroviruses that are abnormally expressed in cancer, neuropathologies or other autoimmune diseases. The present sequence was
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                                                                                                                                                                                                                                                                            Sequence 10499 BP; 3048 A; 2676 C; 2280 G; 2495 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                            Length 10499;
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                                                                                                                                                                                                                                                                                                         Score 505.8; DB 3;
Pred. No. 6.3e-146;
0; Mismatches 42;
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                                                                                                                                                                                                                                                                                                         79.78;
                                                                                                                                                                                                                                                                                                                           Best Local Similarity 91.1
Matches 564; Conservative
                             3; Fig 1; 225pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid sequences of human endogenous retrovirus, HERV-7g, used diagnosis, treatment and prevention of autoimmune and neurological
                                   CGGCAACGGCAACCCCCTTTGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTTTCACTCTA
                                                                            CTGGACCGGCCTGCTAGCCCATGCTCCGATGATGACATTGAAGGCACCCCTCCCGAG
                                                                                                                                        GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
                                                                                                                                                                                                      CATCAGCCAACCTCCCCAACAGCACTTTGGGTTTTTCCTGTTGAGAGGGGGACTGAGAGAC
                                                                                                                                                                                                                                                                  AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
                                                                                                                                                                                                                                                                                                                                GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATTGCCTGAGAGCACAGCGGGAGGGACAAGGATCGGGATATAAACCCCAGGCATTCGAGC
                CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
                                                                                                                                                                                                                                                                                                                                                                                            AGAGAGCTCACTAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7q; immunotherapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABN97929 standard; DNA; 10499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Autoimmune disease; HERV-7q;
multiple sclerosis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-160587/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix. Noteally cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fig.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                         589
                                                                       469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe #4541 for gene expression analysis in human cervical cell sample.
                   279906 AAGACAGCTCACTAAAATGCTAATTAGGCTAAAACAGGAGGTAAAGAAATAGCCAATCA
                                                                                                                                              TCTATTGCCTGAGAGCACAGGGAGGGACAAGGATCGGGATATAAAACCCAGGCATTCGA
                                                                                                                                                                                                                       GCCGGCAACGCCAACCCCCTTTGGGTCCCCTTTGTATGGGCGCTCTGTTTTCACTC
                                                                       --AGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe, human; microarray; gene expression; cervical epithelial cell;
CTGCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATC-
                                                                                                                                                                                                                                                                                                                                      Claim 25; SEQ ID NO 4541; 487pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
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2000US-00632366.
2000US-0234687P.
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2000US-0207456P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cervical cancer; ss
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21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for valuating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vii) for inhibiting the activity of CAP; (vii) for treating carcinoma; (vii) for neutralizing the effect of CAP; (vii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (vii) for treating carcinoma or a propensity to carcinoma; and (xi) for determing Carcinoma Associated (CA) gene copy number. In addition, the CAP genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279786 AGGACTAGCTGGATTTCCTAGGCTGACTAAGAAAATCCCTAAGCCTAGCTGGGAAGGTGA 279845
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTTCCAGAATCAAAACTGTAAAACTA
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                                                                                                          88
                                                                                                      Cytostatic; carcinoma; lymphoma; cancer; human; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1666; Opp; English.
                                                                     Human genomic sequence hCG37193
                                                                                                                                                                                                                                                             28-FEB-2003; 2003WO-US006235
                                                                                                                                                                                                                                                                                                01-MAR-2002; 2002US-00087192
                                 (first entry)
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Matches 577; Conserv
                                                                                                                                                                                    WO2003073826-A2.
                                                                                                                                                  Homo sapiens
                                 18-NOV-2004
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                                                                                                                                                                                                                                                                                                                                                                            Morris DW;
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGGACTGAGAGAC 300
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                                                                                                                                                                                                                                                                                                                                              Score 499.6; DB 4; Length 1894;
Pred. No. 2.3e-144;
0; Mismatches 54; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1894 BP; 557 A; 500 C; 361 G; 476 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 4642; 639pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                            Human genome-derived single exon nucleic gene expression in human fetal liver.
                                                                                               Rank 1
                                                                      (MOLE-) MOLECULAR DYNAMICS INC
                                                                                               Chen W,
          03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234559P.
04-OCT-2000; 2000CB-00024263.
                                                                                                                                                                                                                                                                                                                                                 Query Match 78.7%;
Best Local Similarity 88.7%;
Matches 571; Conservative C
2000US-00608408
                                                                                               Hanzel DK,
                                                                                                                     WPI; 2001-483447/52
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                        Length 1894;
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 C; 361 G; 476 T; 0 U; 0 Other;
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                       'Match 78.7%; Score 499.6; DB 4; Local Similarity 88.7%; Pred. No. 2.3e-144; les 571; Conservative 0; Mismatches 54;
                                                                          CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTC
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26-MAY-2000; 2000US-0207456P.
   A; 500
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  BP; 557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; microarray; single exon probe; gene expression; breast; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived
                                                                                                                                                                                                                              1457 TGTTGGCCAACCTCCCCAACAGCAGTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; 2000US-0180312P.
; 2000US-0207456P.
; 2000US-00608408.
; 2000US-0234687P.
; 2000US-0234887P.
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for prodicting a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1894 BP; 557 A; 500 C; 361 G; 476 T; 0 U; 0 Other;
             Indels
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cisorder; ss.
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Best Local Similarity 88.7%; Pred. No. 2.3e-144;
Matches 571; Conservative 0; Mismatches 54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
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; 2000US-020456P.
; 2000US-0060408.
; 2000US-00632366.
; 2000US-0234687P.
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                                                                                                                              AAI35980 standard; DNA; 1894
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27-SEP-2000;
04-OCT-2000;
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from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genemic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGCAACGGCAACCCCCTTTGGGTCCCCTTTTGTATGGGCGCTCTGTTTTCACTCTA. 591
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                                                                                                                                                                                                                                                                                                                                     Length 1894;
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                                                                                                                                                                                                                                                                                               Sequence 1894 BP; 557 A; 500 C; 361 G; 476 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 571; Conserv
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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived probes are useful for predicting, diagnosing grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                        Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             form part of the printed specification, but was obtained in electronid format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                      expression; heart; microarray; vascular system; probe;
lar disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
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Pred. No. 2.3e-144;
0; Mismatches 54; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1894 BP; 557 A; 500 C; 361 G; 476 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                              DR;
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30-UUN-2000; 2000US-0060B408.
03-AUG-2000; 2000US-0043366.
21-SEP-2000; 2000US-0234369P.
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88.7%;
                                                                      congenital heart disease; ss
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Best Local Similarity 88.79
Warches 571; Conservative
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                                                         cardiovascular
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                                                         241 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTTCCTGTTGAGAGGGGGGACTGAGAGAC 300
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                                                                                                                                                                                                                                                                                                                                                                            CGGCAACGCCATTTGGGTCCCCTTCCTTTGTATGGCCGCTCTGTTTTCACTCTA
                                                                                                                                                                                           TATTGCCTGAGAGCACAGCGGAGGGACAAGGATCGGGATATAAAACCCCAGGCATTCGAGC
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                                                                                                                                 CTGGACCGGCCTGCTAGCCCCATGCTCAATGACATTGAAGGCACCCCTCCCGAG
                                            CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTAAAACTA
                                                                                      CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACGGTGGACCC
                                                                                                                                                                             GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
                      19;
Length 1894;
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  DB 4;
                        54;
 Score 499.6; DB 4;
Pred. No. 2.3e-144;
0; Mismatches 54;
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26-MAY-2000; 2000US-0207456P.
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 78.7%;
nilarity 88.7%;
Conservative 0
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   Query Match
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Matches 571;
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                                                                                                       1696
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   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
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                                                                                                                                            TATTGCTGAGAGCACAGCGGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGC
                                                        AGAGACCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATC
                                                                                                                                                                           CGGCAACGGCAACCCCCTTTGGGTCCCCTTTCTTGTATGGGCGCTCTGTTTTCACTCTA
                                                                                                                                                                                                                                                                                                                                                                                          Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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                                        GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATC-
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                                                                                                                                                                                                                      Rank DR;
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26-WAY-2000; 2000US-0201456P.
30-UJN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000GB-00324559P.
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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult (C measuring human gene expression in a sample derived from human adult (I) were comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABS25011-ABS31005 represent human coronary near disease. ABS25011-ABS31005 represent human coronary near this patent does not appear in the printed sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cccrerarcritaaccrccritraacritricrcritriccagaarcgaaccagraaacra 1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTAAAAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 1894;
                                                                                                                                                                                                                                                         Human, single exon nucleic acid probe; liver; cirrhosis;
hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1894 BP; 557 A; 500 C; 361 G; 476 T; 0 U; 0 Other;
1807 CTTCACTCTATTAAATCTTGCAACTGCAAAAATAAAAATAGAAA 1850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 499.6; DB 4;
Pred. No. 2.3e-144;
0; Mismatches 54;
                                                                                                                                                                                                                      SEQ ID No 4660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 4660; 658pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene expression in human adult liver.
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                                                                                                   ВР
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                                                                                                                                                                                                                      Human liver single exon probe,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen W,
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88.7%;
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
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                                                                                                   DNA; 1894
                                                                                                                                                                                                                                                                                                     coronary heart disease; ss.
                                                                                                                                                                               (first entry)
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Matches 571; Conservative
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                                                                                                   ABS29670 standard;
                                                                                                                                                                                                                                                                                                                                                                               WO200157273-A2
                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2000;
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                                                                                                                                                                               25-FEB-2003
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                                                                                                                                          ABS29670;
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                                                             RESULT ABS29670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1457 TCTTGGCCAACCTCCCCAACAGCAGTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC 1516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1517 AGGAATAACTAGATTTCCTAGACCAACTAAGAATCCCTAAGACTAGCTGGGAAGGTGACC 1576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGCTTGAGAGAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  591
                                                                                                                                                                                                                                                                                                                                                            probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09
                                                                                                                                                                                                                                           exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGCAACGGCAACCCCCTTTGGGTCCCCTTCGTATGGGCGCCTCTGTTTTCACTCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1277 CAAATCGTTCTTCAAATGGAGCCCCAGATGCAGTCCATGAGTAAAATCTACCACGGACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 499.6; DB 4; Length 1894;
Pred. No. 2.3e-144;
0; Mismatches 54; Indels 19;
                                                                                                                                                                                                                                                                                                                                            present invention provides a number of single exon nucleic
                                                                                                                                                                                                                                                                                                     Example 4; SEQ ID NO 4507; 650pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1894 BP; 557 A; 500 C; 361 G; 476 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cacctacacctacctriridesrccccrcctriretaressascrcter
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                                                                                                                                                                 Rank
                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC.
      ; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
; 2000US-0236359P.
                                                                                                                                                                 Chen W,
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                                                                                  04-OCT-2000; 2000GB-00024263
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11, Conservative
                                                                                                                                                                 Hanzel DK,
                                                                                                                                                                                                        WPI; 2001-483446/52
        30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                  27-SEP-2000;
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                                                                                                                                                                                1516
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inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGAAGGTGACT
                                                                                                                                                                                                                                        TATTGCCTGAGAGCACAGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGC
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   cregacceccrecrageccargerregargranargacarregagecaccereceage
                                                                                                          GAAATCTCAACTGCACAACCTCTACTACGCCCCAATTCAGCAGGAAGCAGTTAGAGTGGT
                                                                                                                                              241 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGGACTGAGAGAC
                                                                                                                                                                 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATC-----
                                                                                                                                                                                                                                                                                                                                                              AGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAAATAGAAATAGCCAATCATC
                                                                       GAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used to measure gene expression in human breast sample.
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30-JUN-2000; 2000US-0060B40B.
03-AUG-2000; 2000US-00632466.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-0234589P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI04422 standard; DNA; 1894
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1697 İGTİĞCCİĞACAĞCAĞĞAĞĞĞĞĞĞAÇANTĞATCĞĞĞATITAAAÇCCAĞĞĞATTCĞAĞC 1756
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                          The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe breast. The probes are useful for a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
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78.7%; Score 499.6; DB 5;
Best Local Similarity 88.7%; Pred. No. 2.3e-144;
Matches 571; Conservative 0; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             completed: February 21, 2005, 07:45:38
25; SEQ ID NO 4413; 322pp; English.
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MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 102:
US-08-979-847B-102
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                                                178
176.8
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176.8
175.
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166.8
164.8
156
156
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Sequence 108, App
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Sequence 103638,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50, Appl
                                                                           February 21, 2005, 06:54:34; Search time 111.885 Seconds (without alignments) 9286.612 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17002,
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                                                                                                                                  Description
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                                                                                                                                                                                                                                                                                                                                                                          Issued Patents NA:*

1. /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2. /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3. /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

5. /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5. /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

5. /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6. /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-949-016-17382
US-09-949-016-15858
US-09-949-016-15858
US-09-949-016-13002
US-09-949-016-17411
US-09-949-016-174117
US-09-949-016-17417
US-09-949-016-17497
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US-09-949-016-17399
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US-09-949-016-103637
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                                                                                                                                                                                                                              1202784 segs, 818138359 residues
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                                                     model
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 sv
                                                      - nucleic search, using
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Maximum DB seq length: 200000000
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Match Length DB
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TITLE OF INVENTION: VIERL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHY
THERAPEUTIC PURPOSES
                                                  Sequence 128750,
Sequence 17057, A
Sequence 44301, A
Sequence 195792,
                                                                                                                                                                                     Sequence 13633,
Sequence 11770,
Sequence 11757,
                                                                                                                                                                                                                                           Sequence 15019, 1
Sequence 16278, 1
Sequence 12262, 1
Sequence 202370,
                                                                                                                    17296,
                                                                                                                                                                          Sequence 13413,
                                                                                                                    Sequence Sequence Sequence
                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Ellopy disk
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979, 847B
FILING DATE: 26-No. 6582703-1997
CLASSIFICATION: ¿Unknown>
US-08-721-489-4
US-09-573-080A-21
US-09-573-080A-21
US-09-949-016-128750
US-09-949-016-44301
US-09-949-016-145792
US-09-949-016-145792
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US-09-949-016-11757
US-09-949-016-11757
US-09-949-016-12678
US-09-949-016-12678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: BERRIOGE, WILLIAM P.
REGIGSTATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10.2, Application US/08979847B
Patent No. 6582703
GENERAL INFORMATION:
BESEME, FREDERIC
BEDIN, FREDERIC
BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
MANDRAND, BERNARD
GARGON, JEREMY
TUKE, PHILIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSES: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 635 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 102
SEQUENCE CHARACTERISTICS:
                                                                                                                                        251682
601
116652
39686
49487
131631
57507
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                                         331.0
330.8
330.8
227.8
227.8
227.8
277.5
4.7.5
       233.6
219.6
196.6
195.6
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480
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                                                                           #1.30
                        COURTER FIORY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OFFRARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,847B
FILING DATE: 26-NO. 6582703-1997
CLASSIFICATION: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELEPONUMINACATION INFORMATION:
TELEPONUMINACATION 108-036-2787
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 545; DB 4; 1
Pred. No. 7.2e-173;
0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-08-979-847B-108
                                                                                                                                                                                                                                                                                                 LENGTH: 1329 base pairs
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                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 92.4%;
Matches 572; Conservative (
ZIP: 22320
COMPUTER READABLE FORM:
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GARSON, JEREMY
TUKE, PHILLE
TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
THERAPEUTIC PURPOSES
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                                Gaps
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 Length 635
                                Indels
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    4.
 Score 635; DB 4;
Pred. No. 2e-203;
0; Mismatches (
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BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOMUBLAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 108, Application US/08979847B
Patent No. 6582703
GENERAL INFORMATION:
APPLICANT: PERRON, HERVE
BESSEME, FREDERIC
 Query Match
Best Local Similarity 100.0%;
Matches 635; Conservative 0
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US-08-979-847B-108
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Sequence 17382, Application US/09949016
; Sequence 17382, Application US/09949016
; Patent No. 6812339
; GENERAL INCOMMATION:
    APPLICANT: VENTER, U. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    CURRENT FILING DATE: 2000-04-14
    PRIOR APPLICATION NUMBER: 60/241,755
    PRIOR FILING DATE: 2000-10-20
    PRIOR FILING DATE: 2000-10-03
    PRIOR FILING DATE: 2000-10-08
    PRIOR FILING DATE: 2000-09-08
    NUMBER OF SEQ ID NOS: 207012
    SOFTWARE: FASISEQ for Windows Version 4.0
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                                                     81.3%; Score 516.2; DB 4;
91.1%; Pred. No. 1.7e-162;
ive 0; Mismatches 43;
                      Query Match
Best Local Similarity 91.1
Matches 564; Conservative
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                                                                                                                                                      RESULT 4
US-09-949-016-17382
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APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Freacy, Maurice
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84.1%; Score 533.8; DB 3;
Best Local Similarity 91.5%; Pred. No. 7.2e-169;
Matches 581; Conservative 0; Mismatches 42;
                                                                                                                                                      Sequence 3, Application US/09175928A Patent No. 6312921 GENERAL INFORMATION:
SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 3
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Sequence 1585B, Application US/09949016
; Sequence 1585B, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
    APPLICANT: VBYTER, US/09949, US
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WINDER: US/09/949,016
; CURRENT FILING DATE: 2000-00-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,756
; PRIOR PLING DATE: 2000-10-03
; PRIOR PLING DATE: 2000-10-03
; PRIOR RELING DATE: 2000-0-10-03
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Pred. No. 6e-160;
0; Mismatches 49; Indels 15;
                                                                                                                   2746 ATTAAATCTTGCAACTG 2762
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Best Local Similarity 90.0%;
Matches 575; Conservative
                                                                                        601 ATTAAATCTTGCAACTG
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US-09-949-016-15858/c
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| Sequence Set0, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VEWTER, VEW
                  11459 CAACCCCTTTGGGTCCCCTCTTTGTATGGGAGCTCTGTTTTCATGCTATTTCACCTT 11518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.2%; Score 515.8; DB 4;
llarity 91.2%; Pred. No. 8.1e-163;
Conservative 0; Mismatches 42;
                                                                                                           Best Local Similarity
Matches 563; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                           RESULT 5
US-09-949-016-5640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-949-016-5640
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Sequence 13002/C
; Sequence 13002/C
; Sequence 13002, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VEWTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FREESEQ for Windows Version 4.0
; SEQ ID NO 13002
; LEWGTH: 168394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25144 --GGACCAGCCTGCTAGCCCATGCTCC-AAGTTAATAACATCAAAGGACCTCTCCAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.6%; Score 448; DB 4; Length 168394; 88.7%; Pred. No. 8.4e-139; Live 0; Mismatches 55; Indels 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (1)...(168394)
; OTHER INFORMATION: n = A,T,C or
US-09-949-016-13002
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Matches 534; Conservative
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LOCATION: (1)...(16839
                                                                                                  6180 CTATT 6176
                                                                          CTATT 593
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ORGANISM: Human
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1 Sequence 17411, Application US/09949016

1 Sequence 17411, Application US/09949016

1 PATENT NO. 6812339

1 GENERAL INFORMATION:

2 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

1 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

1 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

2 CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PELING DATE: 2000-10-20

3 PRIOR PELING DATE: 2000-10-03

4 PRIOR PELING DATE: 2000-10-03

5 PRIOR PELING DATE: 2000-09-08

5 NUMBER OF SEQ ID NOS: 207012

5 SOFTWARE: FastSEQ for Windows Version 4.0

5 SEQ ID NO 17411

LENGTH: 99580
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Pred. No. 1.2e-140;
0; Mismatches 55; Indels 12;
                                                                             92007 CTTCACTCTATTAAATATTGCAACTGCAAAAAAAAAAA 91969
                                                               71.3%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.9
Matches 538; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Human
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US-09-949-016-12249/c

US-09-949-016-12249, Application US/09949016

Sequence 12249, Application US/09949016

Sequence 12249, Application US/09949016

SEQUENCE 12249, Application US/09949016

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLOOL307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PELING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-01-03

PRIOR PELING DATE: 2000-01-03

PRIOR PELING DATE: 2000-01-03

SPRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

SPRIOR PRIOR 
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Pred. No. 3.4e-137;
0; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (1)...(77997)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 69.7%;
Best Local Similarity 88.9%;
Matches 538; Conservative C
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ORGANISM: Human
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US-09-949-016-17417/c

j Sequence 17417, Application US/09949016

j Edent No. 681233

j GENERAL INFORMATION:
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

j TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

j TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

j TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

j TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

j TITLE OF INVENTION: WIMBER: 60/241,755

PRIOR PELLING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PELLING DATE: 2000-10-03

PRIOR PELLING DATE: 2000-10-03

PRIOR PELLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

sSOCIWARE: FEBELSOR

LENGTH: 77772
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24728 TGGCAATGGCTACCCTCTTTGGGTCCCCTCCTTTGTATGGGAGCTCTGTTTTCACTCTA 24669
                    14848 AGAGAGTICACIAAAATGCTAACTAGGCAAAAACAGGAGGTAAAGAAATAGCCAATCAIC 24789
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                                                                                                        69.7%; Score 442.6; DB 4; Length 77772; 88.9%; Pred. No. 3.4e-137; tive 0; Mismatches 54; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (1)...(77772)
; OTHER INFORMATION: n = A,T,C or
US-09-949-016-17417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.9
Matches 538; Conservative
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Sequence 13590, Application US/09949016

Sequence 13590, Application US/09949016

Setent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER: OF SEQ ID NOS: 207012

SEQ ID NO 13590

LENGTH: 149971
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                                                                                        TATTGCCTGAGAGCACAGCGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGC 531
                                                                                                                                                       239 GTCATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAG
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Pred. No. 1.4e-111;
0; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (1)...(149971)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13590
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Best Local Similarity 80.9%;
Matches 529; Conservative (
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; Sequence 44300, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    FILE REFERENCE: CLOOD.307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT PILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; ROSTWARE: PRESENCE OF WINDOWS Version 4.0
; SGO ID NO 44300
; LENGTH: 601
             15617 CACACCCACTTTAAACATGGGGCTTGTAACTCAGCTCACACAAACATAGTA 15558
                                                                                                                                              15437 AGCCGAATCGGGCAACCCTCTTTGGGTCCCCTCCGGTTGCATGGGAGCTCTGTTTTCACG 15378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --GGACCAGCCTGCTAGCCCATGCTCC-AAGTTAATAACATCAAAGGCACCTCTCCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               492 CAAATTGTTCTACAATGGAGCCCCAGATGCAGTCCATGACTAAAATCTACTGCAGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
                                                                                                                                                                                                                                                              529 AGCCGGCAACGCCAACCCCCTTTGGGTCCCCTTCGTATGGGCGCTCTGTTTTCACT
                                                                                                                             412 -AGAGAGCTCACTAAAATGCTAATTAGGC-AAAAATAGGAGGTAAAGAAATAGCCA-ATC
                                                            360 IGCATCCACCICIAAACAIGGGGCTIGCAACTIAGCTCACACCCGACCAAIC-----
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Pred.. No. 5e-126;
1; Mismatches 52; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 63.8%;
Best Local Similarity 88.1%;
Matches 489; Conservative
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                                                                                                                                                                                                                                                                                                                                  589 CTATT 593
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US-09-949-016-44300/c
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; ORGANISM: Human
US-09-949-016-44300
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US-09-949-016-133739/c

| Sequence 133739, Application US/09949016
| Patent No. 6812339, Application US/09949016
| Patent No. 6812339, Application US/09949016
| Patent No. 6812319, Application In Version In Ve
142217 cadecadeaacedenacacretrifederecetrecetrinararegeaecreferriceae 142158
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                                                                           CCCCTCCCTTTGTATGGGCGCTCTGTTTTCAC
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US-09-949-016-15393
US-09-949-016-15393, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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pred. No. 1.2e-87;
1; Mismatches 25;
                                                                                                                                                                                                    142157 TCTATTTCACTCTATTAAATCTTGCAACTGCA 142126
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92.2%;
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US-09-949-016-133739
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Best Local Simi
Matches 306;
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; Sequence 15497, Application US/09949016
; Batent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; CURRENT APPLICATION NUMBER: 60/241,755
; CURRENT APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FRAESEQ for Windows Version 4.0
; SEQ ID NO 15497
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                                                                                                         18459 ACAAGACTAGCTGGATTTCCTAAGCGGCTAAGAATTCCTAAACCCAGCTGGGAAGGTGA 18400
                                                                                                                                                                                        18519 GTCGTCGGCCAACCTCCCCAACAGCACTTGAGTTTTCCTGTTGAGAGCCGAGACTGAGAG 18460
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                                                                                                                                                            CTGCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCGACCAATC-----
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46.0%; Score 292; DB 4; Length 245286;
Best Local Similarity 92.5%; Pred. No. 4.2e-86;
Matches 307; Conservative 0; Mismatches 25; Indels 0;
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OTHER INFORMATION: n = A,T,C or
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15086
                                                                                     TYPE: DNA
ORGANISM: Human
                                                                                                                       ; OKGANISM: Human
US-09-949-016-44296
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Sequence 44296, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PLILNG DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-08
RIOR FILING DATE: 2000-10-09
RIOR FILING DATE: 2000-10-08
RIOR FILING DATE: 2000-10-09
RIOR FILING DATE: 2000-10-09
RIOR FILING DATE: 2000-10-09
RIOR FILING DATE: 2000-10-09
RIOR FILING DATE: 2000-10-09
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RIOR FILING DATE: 2000-10-09
RIOR FILING DATE: 2000-10-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 IGGATITCCTAGGCCAACGAAGAATCCCTAAGCCTAGCT-GGGAAGGIGACTGCAICCAC 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGAGAGCACAGCGGGGGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAA 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 288; DB 4;
Pred. No. 8.1e-85;
0; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 82.6%;
Matches 393; Conservative
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US-09-94-016-15086/C

Sequence 15086, Application US/09949016

Patent No. 6812339

Patent No. 6812339

TUTLE VERIBEAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WIMBER: US/09/949,016

CURRENT PELLING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR PELLING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR SEQ ID NOS: 207012

SOFTWARE: PRESENCE for Windows Version 4.0

SEQ ID NO 15086
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                                                                                                                                                                       Length 601;
                                                                                                                                                                                                                     Indels
                                                                                                                                                                     43.0%; Score 273.2; DB 4;
85.5%; Pred. No. 1.9e-81;
ive 1; Mismatches 49;
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 44296
LENGTH: 601
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Matches 376; Conservative
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Best Local Similarity
Matches 281; Conserva
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RESULT 19
US-09-949-016-103638/c
j Sequence 103638 Application US/09949016
j Batent No. 6812339
j GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
PRIOR REPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PLING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
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                                               523
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CAATCATCTATTGCCTGAGAGCACAGGGAGGACAAGGATCGGGATATAAACCCAGGC
                                                                          181 CAATCATCTATCGCCTGAGAGCACAGGGGGGGGGACAATGATCGGGATATAAACCCAGGC
                                                                                                            ATTCGAGCCGGCAACGCCAACCCCTTTGGGTCCCCTTTGTATGGGCGCTCTGTTT
                                                                                                                            241 ATTCGAGCCGGCAACGGCTACCCTCTTGGGTCCCCTCTTGTATGGGAGCTCTGTTT
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Pred. No. 2.3e-74;
1; Mismatches 29;
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US-09-949-016-103639/c
; Sequence 103639, Application US/09949016
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86.3%;
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Best Local Similarity 86.3
Matches 308; Conservative
                                                                                                                                                                                             TCACTCTATT 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-103638
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US-09-573-080A-385
Sequence 385, Application US/09573080A
Patent No. 6828097
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
PILE REFERENCE: 30307
CURRENT FILING DATE: 2000-05-16
CURRENT FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 479
SOFTWARE: Patentin version 3.0
SEQ ID NO 385
LENGTH: 780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411
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                                                                         412
                                                                                                                                      472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 TGAGAGACAGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGA
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                              AGGIGACTGCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCA
                                                                                                                                      413 GAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCT
                                                                                                                                                                                                 473 ATTGCCTGAGAGCACAGCGGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: rerpeat region
LOCATION: (1)...(780)
OTHER INFORMATION: ltr17
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A
TITLE: Prototypic sequences for human repetitive DNA
JOURNAL: Journal of Molecular Evolution
                                                                                                                                                                                                                                                                                                                                                            92254 T 92254
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PAGES: 286-291
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US-09-573-080A-385
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Best Local Simi
Matches 289;
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Sequence 1466B, Application US/09949016

Sequence 1466B, Application US/09949016

Patent No. 6812339

CENERAL INFORMATION:
PITLE DO INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastesQ for Windows Version 4.0

SEQ ID NO 14608

LENGTH: 256287

PUBLICATION NUMBER: 60/2877
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Best Local Similarity 86.3%; Pred. No. 2.9e-72;
Matches 308; Conservative 0; Mismatches 30; Indels 19;
                                                   39.5%; Score 251; DB 4; Length 601;
86.3%; Pred. No. 5.7e-74;
tive 0; Mismatches 30; Indels
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14608
                                                         Query Match
Best Local Similarity 86.33
Matches 308; Conservative
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ORGANISM: Human
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US-09-949-016-103637
ORGANISM: Human
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| Sequence 103637, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER, U. Craig et al. |
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; FILE REFRENCE: CLOR01307 |
| CURRENT APPLICATION NUMBER: US/09/949,016 |
| CURRENT APPLICATION NUMBER: 60/241,755 |
| PRIOR APPLICATION NUMBER: 60/241,755 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-09-08 |
| NUMBER OF SEQ ID NOS: 207012 |
| SOFTWARE: FESESEQ FOR Windows Version 4.0 |
| SOFTWARE: FESESEQ FOR Windows Version 4.0 |
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANTON NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTUM OF SEQ ID NOS: 207012
SEQ ID NO 103639
LENGTH: 601
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Best Local Similarity 86.3%;
Matches 308; Conservative
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US-09-949-016-103637/c
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; ORGANISM: Human
US-09-949-016-103639
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LENGTH: 601
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Sequence 17420, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICATY: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/21,455
PRIOR APPLICATION NUMBER: 60/21,498
PRIOR FILING DATE: 2000-10-03
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FESTSEQ for Windows Version 4.0
SEQ ID NO 17420
LENGTH: 84571
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Sequence 17002, Application US/09949016

Bateat No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF INVENTION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-09

PRIOR FILING DATE: 2000-09-08
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Pred. No. 8e-71;
0; Mismatches 22;
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LOCATION: (1)...(84571)

CTHER INFORMATION: n = A,T,C or G

US-09-949-016-17420
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Best Local Similarity 99.4%;
Matches 303; Conservative
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US-09-949-016-17002
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| Sequence 44299, Application US/09949016
| Sequence 44299, Application US/09949016
| Patent No. 681239
| GENERAL INFORMATION |
| TITLE OF INVENTION |
| TITLE OF INVENTION | WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION | WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION | WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION | WINBER: US/09/949,016 |
| CURRENT APPLICATION NUMBER: 60/241,755 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-09-08 |
| NUMBER OF SEQ ID NOS: 207012 |
| SOFTHARE: FASEEGE FOR WINGOWS Version 4.0 |
| LENGTH: 601
                                                                                                                                                                                                                                                                                           116237 GTÁGCCAATCATCTGTCGCCTGAGAGCACAGGGGGGGGGACAATGATGATCAGGATATAAACC 116178
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                     408 AATC-----AGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAA
                                                                                                                                     459 ATAGCCAATCATCTATTGCCTGAGAGCACAGGGAGGACAAGGATCGGGATATAAACC
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Best Local Similarity 88.5
Matches 284; Conservative
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US-09-949-016-44299/c
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ORGANISM: Human
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RESULT 24 US-09-949-016-17420

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Length 84571; Indels 349

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65951 TGGGAAGGTGATCACATCCACCTTTAAACATGGGGCTTACAACTTAGCTCACACCCGACC 65892
                                                                                                                                       65891 AATCAGGTAAAGAGAGCTCACTAAAATGCTAATTAGGCATAA--AGGAGGTAAAGAA 65834
                                                                                                                                                                                                              459 ATAGCCAATCATCTTTGCCTGAGAGCACAGGGGAGGGACAAGGATCGGGATATAAACC
                                                                                                                                                                                                                                                                              408 AATCAG-----AGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: McCoy, John
APPLICANT: LaVallie, Edward
APPLICANT: Racie, LaVallie, Edward
APPLICANT: Racie, David
APPLICANT: McDerg, David
APPLICANT: Treacy, Maurice
APPLICANT: Fanns, Cheryl
APPLICANT: Spans, Cheryl
APPLICANT: Spans, Cheryl
APPLICANT: Spansiding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPATURE: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 233.6; DB 1;
Pred. No. 2.6e-68;
1; Mismatches 32;
                  348 TGGGAAGGTGACTGCATCCACCTCTAAACATGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/686,878A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 50, Application US/08686878A
Patent No. 5708157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INPORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 279 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                            65713 idriricaciciari 65699
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88.1%;
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Best Local Similarity 88.1
Matches 245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02140
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; Sequence 17068, Application US/09949016
; Sequence 17068, Application US/09949016
; Patent No. 681233
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; FILE REFERENCE: CL00.307
; CURRENT APPLICATION NUMBER: 06/241,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,498
; PRIOR PELLING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-00-08
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SEQ ID NOS: 207012
; SEQ ID NO 1068
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                                                                                                                                                                                                                                                                                                                                                                                                                                            339 AAGCCTAGCTGGGAAGGTGACTGCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Gaps
                                                                                                                                                                                                                                                              38.7%; Score 245.6; DB 4; Length 140224; 86.9%; Pred. No. 1.3e-70; tive 0; Mismatches 34; Indels 9; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.7%; Score 239.4; DB 4; Length 89584;
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NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                       ) NAME/KEY: misc_feature

) LOCATION: (1)...(140224)

) OTHER INFORMATION: n = A,T,C or G

US-09-949-016-17002
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Matches 283; Conservative
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 86.95
Matches 285; Conservative
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; ORGANISM: Human
US-09-949-016-17068
                                                                                       TYPE: DNA
ORGANISM: Human
                                           SEQ ID NO 17002
LENGTH: 140224
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                                                                                                                                                                                                                                                                                                             CGGCAACCCCTTTGGGTCCCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCAC 597
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1 RCCACATCCACCTTTAAACACGGGGNTTGCAAANAAGATNACACTTGACCAATCAGAGAG
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                                                                   118 CTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATTGC
                                                                                                                                                                                          CTGAGAGCACAGCGGGAGGGACAAGGATCGGGGATATAAACCCAGGCATTCGAGCCGGCAA
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LOCATION: (1)..(8523)
OTHER INFORMATION: herv17
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A
TITLE: Prototypic sequences for human repetitive DNA
JOURNAL: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTATTAAATCTTGCAACTGAAAAAAAAAAAAAAAA. 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 INTATTAAATNITGCAACTGCAAAAAAAAAAAAAA 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: JOAN, KNOLL
APPLICANT: ROGAN, PETER
TITLE OP INVENTION: SINGLE COPY GENOMIC FILE REFERENCE: 30307
CURRENT APPLICATION NUMBER: US/09/573,080A
CURRENT FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . Sequence 21, Application US/09573080A; Patent No. 6828097; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISSUE: 4
PAGES: 286-291
DATE: 1992-10-
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SEQ ID NO 21
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                                                                                                                                             477
                                                                                                                                                                                          61 NICANTAAAATGATNATTNGGCAAAAACAGGAGGAAAGAAATAGCCAATCATCATTGC 120
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                                                                                                                                                                                                                                                                                                                                                                                       CGGCAACCCCCTTTGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCAC
                         ACTGCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAG
                                                                   1 RCCACATCCACCTTTAAACACGGGGNTTGCAAANAAGATNACACTTGACCAATCAGAGAG
                                                                                                                                             418 CTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGC
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APPLICANT: LaValle, Edward
APPLICANT: LaValle, Edward
APPLICANT: Racie, Lisa
APPLICANT: Merberg, David
APPLICANT: Tractor, Maurice
APPLICANT: Tractor, Maurice
APPLICANT: SPANISHON, SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEB: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 INTATTAAATNITGCAACTGCAAAAAAAAAAAAAAAA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/721,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 233.6; DB 1;
Pred. No. 2.6e-68;
1; Mismatches 32;
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NAME: Brown, Scott A.
REGISTRATION UNMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-824
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 279 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08721489 Patent No. 5786465
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ilarity 88.1%;
Conservative
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TYPE: nucleic acid
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Best Local Similarity
Matches 245; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: CDNA US-08-721-489-4
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US-08-721-489-4
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Indels

Length 601;

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Sequence 17057, Application US/09949016

Sequence 17057, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,768

PRIOR APPLICATION NUMBER: 60/231,498

SEQUENCE APPLICATION NUMBER: 60/231,498

SEQUENCE APPLICATION NUMBER: 60/231,498

SEQUENCE APPLICATION NUMBER: 60/231,498

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SEQUENCE APPLICATION NUMBER: 60/231,498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 Achigcacaacccracrargcccccagricaccacaaacaaacaarraaacaarrargccca 361
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                                                                                                                                                                                                                                                                                                                      130 CCTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAGGAAATCTCA
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28.4%; Score 180.4; DB 4; Length 1.
Best Local Similarity 82.1%; Pred. No. 1.3e-48;
Matches 271; Conservative 0; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         420 CACTAAAATGCTAATTAGGC-AAAAATAGGAGGTAAAGAAATAGCCAA
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80.5%; Pred. No. 2.7e-55;
iive 1; Mismatches 55;
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 128750 LENGTH: 601
                                                                                                                                                                                                                                                                   Matches 280; Conservative
                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                   US-09-949-016-128750
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; ORGANISM: Human
US-09-949-016-17057
                                                                                             TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                369
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; Sequence 128750, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WHOMER: 60/29,949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292 CTGAGAGACAGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGG 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 AAGGTGACCACATCCACCTTTAAGCAGGGGCTTGCAACTTAGCTCACACCCGACCAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  523 CATICGAGCCGCCAACGGCAACCCCTTIGGGTCCCCTCCTTIGIAGGGCGCTCTGIT
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                                                                           8472 CGTCGGCCAACCTCCCCAACACTTAGGTTTTCCTGTTGAGATGGGGGAC 8523
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                                                                                                                                                                                             US-09-621-976-9366/C
; Sequence 9366, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: UDmas Milne Edwards, J.B.
; APPLICANT: JODert, S.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; CURRENT FILIGATION NUMBER: US/09/621,976
; CURRENT FILIG DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 9466
; LENDTH: 456
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Pred. No. 1.1e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 84.9%;
Matches 264; Conservative
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CORGANISM: Homo sapiens
US-09-621-976-9366
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419 540

13; Gaps

Length 154023;

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Sequence 17296, Application US/09949016

Sequence 17296, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
TUTLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTHARE: FESTSEQ for Windows Version 4.0

LENTH: 251672
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT PLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PELING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASSEQ for Windows Version 4.0
SEQ ID NO 195792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               351 GAAGGIGACTGCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAAT 410
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                                                                                                                                                                                                                                                                                                                                                                                  Length 601;
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                  27.8%; Score 176.8; DB 4;
85.4%; Pred. No. 6e-49;
iive 0; Mismatches 32;
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Best Local Similarity 85.4'
Matches 270; Conservative
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US-09-949-016-195792
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US-09-949-016-17296
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FEATURE:
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US-09-949-016-44301/c
; Sequence 41301, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
TITLE OF INVENTION: POLYMOREHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOU1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR PILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 44301
LENGTH: 601
                                                          92354 AGGTAATAAAAAAGTCATTAAAATACCAATTAGGCTAAAAGCAGGAGGAGTAAAGAAATA 92413
                                                                                                                                                                             61 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC 120
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Pred. No. 2.4e-49;
0; Mismatches 25; Indels
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US-09-949-016-195792/c
; Sequence 195792, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
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88.5%;
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Best Local Similarity 88.5
Matches 216; Conservative
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ORGANISM: Human
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GENERAL INFORMATION:

JAPPLICANT: VENTER,

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 44110

LENGTH: 601
                                                               42753 CAGGTAGTAAAGAGGCTCACTAAATACAAATTAGGCTAAGAGCAGGAGGTAAAGAAAT 42812
                                                                                                                                                                           42813 AGTCAAATCATCTATCATCTGAGAGCACAGGGGGGGGACAATGATTGGGATATAAACCC 42872
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Pred. No. 2.4e-48;
1; Mismatches 41;
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psquence 44310, Application US/09949016; Patent No. 681233
patent NoroRMATION:
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Best Local Similarity 82.6
Matches 262; Conservative
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ORGANISM: Human
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; Sequence 11973, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; TURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR PLING DATE: 2000-10-03
; PRIOR PLING DATE: 2000-10-03
; PRIOR PLING DATE: 2000-10-03
; PRIOR PELING DATE: 2000-10-03
; PRIOR PELING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR SPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR PRING DATE: 2000-10-03
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                                                                                                                                                                                                                                                                                                                                  351 GAAGGTGACTGCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAAT
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                                                                                                        Length 251672;
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                                                                                                     Score 176.8; DB 4;
Pred. No. 3e-47;
0; Mismatches 32;
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| LOCATION: (1)...(251682)

| OTHER INFORMATION: n = A,T,C or G

US-09-949-016-11973

// LOCATION: (1)...(251672)
// OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17296

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                                                                                                        Query Match
Best Local Similarity 85.4%;
Matches 270; Conservative (
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US-09-949-016-11973
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13;

Length 39686;

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Sequence 11770, Application US/09949016

Sequence 1170, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WIMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASESEQ for Windows Version 4.0

SEQ ID NO 11770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6581 CTCAAATCATCTATCATCTGAGAGGCACAGAGGGACAATGATTGGGATATAAACCCC 6522
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                                                                                                                                                                                                                                                                                                                                               40; Indels
                                                                                                                                                                                                                                                                                                   Query Match

27.4%; Score 174; DB 4;
Best Local Similarity 83.1%; Pred. No. 7.9e-47;
Matches 261; Conservative 0; Mismatches 40.
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13633
LENGTH: 39686
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; OTHER INFORMATION: n = A,T,C or
US-09-949-016-11770
                                                                                                                                                                     FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(39686)
CTHER INFORMATION: n = A,T,C or ()
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83.1%;
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Best Local Similarity
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ORGANISM: Human
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ORGANISM: Human
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                   Jequence 13413, Application US/09949016

| Sequence 13413, Application US/09949016
| Patent No. 681239
| GENERAL INFORMATION:
| APPLICANT' ENTER: VENTER, VICTAIG et al.
| APPLICANT' ENTER: VICTAIGN WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| TITLE OF INVENTION NUMBER: 60/241,755
| PRIOR PILING DATE: 2000-10-20
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 13413
| LANGOTH: 116652
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| Sequence 13633, Application US/09949016
| Sequence 13633, Application US/09949016
| Sequence 13633, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| CURRENT APPLICATION NUMBER: 05/09/949,016
| CURRENT FILING DATE: 2000-04-14
| PRIOR PELLING DATE: 2000-10-20
| PRIOR PELLING DATE: 2000-10-30
| PRIOR FILING DATE: 2000-10-33
| PRIOR PLING DATE: 2000-10-33
| PRIOR PELLING DATE: 2000-10-33
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Pred. No. 1e-46;
0; Mismatches 34; Indels 14;
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US-09-949-016-13413
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Best Local Similarity 84.9%;
Matches 269; Conservative
                     US-09-949-016-13413/c
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ORGANISM: Human
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q _C	16091	TGAGAGGCAGGACTAGCTGGATTTCCTAGGCCGACTAAGAATTCCTAAGCCTAGCTGGGG 15992
à	352	AAGGTGACTGCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACCACCGACCAATC 411
d d	15991	15991 AAGGTGACTGCACCTTTAAACACGGGGCTTGTAACTCAGCTCACTCGACTCAATC 15932
à	412	AGAGAGCTCACTAAAATGCTAATTAGG-CAAAAATAGGAGGTAAAGAAATA 461
e e	15931	15931 AGGTGGTAAAGAGGCTCACTAAAATATCAATTAGGTTAAAAGCAGGGGGTAAAGAATA 15872
à	462	-GCCAATCATCTATTGCCTGAGAGCACAGGGAGGAGAGAGGATAGGATAAA-CCC 519
ą d	15871	15871 CTCAAATCTTCTATCATCTGAGAGCACAGGGGAGCACAATGATTGGGATATAAACCCC 15812
à	520	520 AGGCATTCGAGCCGGCAACGGCAACCCCTTTGGGTCCCCTCCCT
QQ Q	15811	
ò	580	GTTTTCACTCTATT 593
qq	15751	

Search completed: February 21, 2005, 15:01:18 Job time : 120.885 secs

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Sequence 103, App
Sequence 19, Appl
Sequence 6792, Ap
Sequence 108, App
Sequence 108, App
Sequence 110, App
Sequence 114, App
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
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                                                                                                                                                                                                                                                              February 21, 2005, 11:52:50 ; Search time 350.955 Seconds (without alignments)
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(cgn2_6/ptodata1/pubpna/USO6_PUBCOMB.seq:*
(cgn2_6/ptodata1/pubpna/USO6_PUBCOMB.seq:*
(cgn2_6/ptodata1/pubpna/USO6_PUBCOMB.seq:*
(cgn2_6/ptodata1/pubpna/USO7_NEW_PUB.seq:*
(cgn2_6/ptodata1/pubpna/USO8_PUBCOMB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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6 US-10-114-104-102
1 US-10-637-565-18
8 US-10-719-993-6792
7 US-10-416-642-4
1 US-08-979-847-108
6 US-10-114-104-108
3 US-10-087-192-910
3 US-10-114-893-134
5 US-09-731-231A-3
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                                                                                                                                                                                OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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c 12 532.8 83.9 326014 18 US-10-751-985-3 Sequence 23, Appli 522.8 82.3 283351 18 US-10-719-993-7055 Sequence 23, Appli 522.8 82.3 283351 18 US-10-719-993-7055 Sequence 17995, A 15 522.8 82.3 283351 19 US-10-719-993-6815 Sequence 17995, A 252.8 82.3 1980090 19 US-10-719-993-6815 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 17676, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177, A 17 Sequence 177,
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ALIGNMENTS

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RESULT 1

Sequence 102, Application US/08979847

Publication No. US20030039664A1

GENERAL INFORMATION:
APPLICANT: BESENGE REBERIC
APPLICANT: BESIN, FREDERIC
APPLICANT: WANDEAND. BERNARD
APPLICANT: COLUMBRADE REPRESSION
APPLICANT: COLUMBRAD BERNARD
APPLICANT: THES, PHILIP
APPLICANT: THES, PHILIP
APPLICANT: THES, PHILIP
APPLICANT: THES, PHILIP
APPLICANT: THES, PHILIP
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APPLICANT: THES, PHILIP
APPLICANT: THES, PHILIP
APPLICANT: THES, PHILIP
APPLICANT: THE OF INVENTION: ASCOLATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLA
TITLE OF INVENTION: ASCOLATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLA
TITLE OF INVENTION: ASCOLATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLA
TITLE OF INVENTION: ASCOLATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLA
TITLE OF INVENTION: ASCOLATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLA
TITLE OF INVENTION: ASCOLATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLA
TITLE OF INVENTION: ASCOLATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLA
TITLE OF THE PROPHYLE FORM:
STREET: P.O. BOX 19928
CONNERS: THE PC COMPATIEN FELSOR'MS-DOS
OFFRARET IN PC COMPATIEN FELSOR'MS-DOS
OFFRARET APPLICANTON NUMBER: US/08/979,847
FILING APPLICANTON NUMBER: US/08/979,847
FILING APPLICANTON NUMBER: US/08/979,447
FILING APPLICANTON AND ASSET PROPHYLAS
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                                                                                                                                                                                  Length 635,
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Best Local Similarity 100.0%; Pred. No. 2.4e-187;
Matches 635; Conservative 0; Mismatches 0;
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                                   39046A
        NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERRNCE/DOCKET NUMBER: WPB 39-
TELECOMMUNICATION INFORMATION:
TELEPAN: 703-836-6400
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 635 base pairs
LENGTH: 635 base pairs
TYPE: Nucleic acid
STRANDEDNESS: single
                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA
ATTORNEY/AGENT
NAME: BERRID
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Sequence 102, Application US/10114104 Publication No. US20030198647A1 GENERAL INFORMATION:

10-114-104-102

RESULT 2 US-10-114 APPLICANT: PERRON, HERVE BESEME, FREDERIC BEDIN, FREDERIC

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TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHY)
THERAPEUTIC PURPOSES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FULL.

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/10/114,104

FILING DATE: 03-Apr-2002

CLASSIPICATION NUMBER: 08/979,847

FILING DATE: 26-NOV-1997

ATTORNEY/AGENT INFORMATION:

NAME: BERRIDGE, MILLIAM P.

REDIERRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: 30,024

REFERENCE/DOCKET NUMBER: 30,024

REFERENCE/DOCKET NUMBER: 30,024

REFERENCE/DOCKET NUMBER: 30,024

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REFERENCE/DOCKET NUMBER: 30,024

REFERENCE/DOCKET NUMBER: 30,024

REPERENCE/DOCKET NUMBER: 30,024

REJERAX: 703-836-6400

TELEPAX: 703-836-6400

TELEPAX: 703-836-6400

TELEPAX: 703-836-6400

TELEPAX: 703-836-6200

TELEPAX: 703-836-6400

TELEPAX: 703-836-6400

TELEPAX: 703-836-6300

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TELEPAX: 703-83
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 210
CORRESPONDENCE SADRESS:
ADDRESSES: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 223A
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                COLETTE
                                                         JOLIVET-REYNAUD, CC
MANDRAND, BERNARD
GARSON, JEREMY
TUKE, PHILIP
PARANHOS-BACCALA,
KOMURIAN-PRADEL,
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NAME/KEY: misc_feature
LOCATION: (1)._.(366710)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6792, Application US/10719993

Publication No. US20040265849A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: CARCILL, Michele et al.

TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001496

CURRENT APPLICATION NUMBER: US/10/719,993

CURRENT FILING DATE: 2003-11-24

NUMBER OF SEQ ID NOS: 55342

SOSTWARE FARENCE: FARENCE FOR Mindows Version 4.0
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                                                     481 AGAGCACAGCGGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
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                                                                                                                               361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
                                                                                                                                                    1756 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
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88.9%; Score 564.8; DB 18;
Best Local Similarity 93.4%; Pred. No. 3.9e-164;
Matches 590; Conservative 0; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1996 ATTAAATCTTGCAACTGAAAAAAAAAAAAAAAA 2030
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US-10-719-993-6792/c
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LENGTH: 366710
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US-10-637-565-18
is Sequence 18, Application US/10637565
is Publication No. US20040043381A1
is GENERAL INFORMATION:
is APPLICANT: PARANHOS-BACCALA, Glaucia
is APPLICANT: PERRON, Herve
is APPLICANT: ROWURIAN-PRADEL, Florence
is APPLICANT: ROWURIAN-PRADEL, Florence
is APPLICANT: ROWURIAN-PRADEL, Florence
is APPLICANT: ACMURIAN-PRADEL, Florence
is TITLE OF INVENTION: METHODS FOR DETECTING MSRV-1 RETROVIRUS
is FILE REFERENCE: 110.557
is CURRENT APPLICATION NUMBER: US/10/637,565
is CURRENT FILING DATE: 2003-08-11
is PRIOR APPLICATION NUMBER: PCT/1800/00159
is PRIOR APPLICATION NUMBER: PCT/1800/00159
is PRIOR FILING DATE: 2000-02-15
is PRIOR FILING DATE: 2000-02-15
is PRIOR FILING DATE: 2000-02-15
is NUMBER OF SEQ ID NOS: 20
is SOFTWARE: Patentin version 3.0
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Pred. No. 1.3e-181;
0; Mismatches 11; Indels 0;
                                                                                                                                                                                                                                                                                                                                            601 ATTAAATCTTGCAACTGAAAAAAAAAAAAAAAAAAA 635
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Best Local Similarity 98.3%;
Matches 624; Conservative C
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; LOCATION: (1)
US-10-637-565-18
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LENGTH: 2030
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APPLICANT: PARANHOS-BACCALA, GLAUCIA
APPLICANT: KOMNIAN-PRADEL, FLORENCE
APPLICANT: JOLIVET-REYNAUD, COLETTE
APPLICANT: MANDRAND, BERNARD
APPLICANT: TURE, PHILIP
TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT
TITLE OF INVENTION: THERAPEUTIC PURPOSES
NUMBER OF SEQUENCES: 210
                                                                                                  1699 cercadreacerececaacadeacridddriricereridadadddddadadadadae 1758
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AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
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                                                                                                                                                                                                                             GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,847
FILING DATE: 26-NOV-1997
CLASSIFICATION: 435
ATYONNEY/AGENT INPOMPATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFRENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAK: 703-836-6400
TELEFRAK: 703-836-5787
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BESEME, FREDERIC
BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 108, Application US/08979847
Publication No. US20030039664A1
GENERAL INFORMATION:
APPLICANT: PERROW, HERVE
APPLICANT: BESIME, FREDERIC
APPLICANT: BEDIN, FREDERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTAMATCTTGCAACTG 617
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F: P.O. BOX 19928
ALEXANDRIA
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            13659 CATCAGCCAACCTCACCAACAGCACTTGGGTTTTCCTGTTGAGAGAGGGGACTGAGAGAC 43600
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                                                                                                                                                        541 CAACCCCTTTGGGTCCCCTTCCTTTGTATGGGGGCTCTGTTTTCACTCTATTTCACTCT
                                                                                         13599 AGGACTAGCTGGATTTCCTAGGCCGATTAAGAATCCCTAAACCTAGCTGGGAAGGTGACC
                                                                                                                                   GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
                                                                                                                                                                                                                421 ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
                                                                                                                                                                                                                                                                                              481 AGAGCACAGCGGGAGGGACAAGGATCGGGATATAAACCCCAGGCATTCGAGCCGGCAACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Incyte ID No. US20040043452A1 7477736CB1
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Publication No. US20040043452A1

GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: RAMKUMAR, Jayalaxmi
APPLICANT: RAMKUMAR, Jayalaxmi
APPLICANT: ARVIZU, Chandra
TITLE REFERENCE: PF-0842 PCT
CURRENT APPLICATION NUMBER: US/10/416,642

CURRENT FILING DATE: 2003-05-13
PRIOR APPLICATION NUMBER: 60/249,407

FILING DATE: 2000-11-15

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PERL PROGram
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Pred. No. 1.9e-159;
0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13299 ATTAAATCTTGCAACTGAAAAAAAAAAAAAA 43268
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; OTHER INFORMATION: a, t, c, g, or other
US-10-416-642-4
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93.8%;
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Best Local Similarity 93.8
Matches 579; Conservative
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LENGTH: 2074
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ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYT
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                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
COFFARATION SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NHBER: US/10/114,104
FILING DATE: 03-Apt-2002
CLASSIFICATION: <unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 545; DB 16;
Pred. No. 4.3e-159;
0; Mismatches 47;
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,847
FILING DATE: 26-NOV-1997
ATTORNEY,AGENT INFORMATION:
NAME: BERRIGGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERRICE,DOCKET NUMBER: WPB 39046A
                  OF SEQUENCES: 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-10-114-104-108
                                                                   PLC
                                  NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE,
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION
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INFORMATION FOR SEQ ID NO: 108:
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STRANDEDNESS: single
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92.4%;
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Matches 572; Conservative
                                                                                                               STATE: VA
COUNTRY: US
ZIP: 22320
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                                                                                                                                                                                 ö
                                                                                                                                                    Length 1329;
                                                                                                                                                                                 Indels
                                                                                                                                                                  4.3e-159;
                                                                                                                                                     DB 8;
                                                                                                                                                    85.8%; Score 545; DB 92.4%; Pred. No. 4.3e
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BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
JOLIVET-RESYRAUD, COLETTE
MANDRAND, BERNARD
GARSON, JERBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 108, Application US/10114104
Publication No. USZ0030198647A1
GENERAL INFORMATION:
APPLICANT: PERRON, HERVE
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ATTAAATCATGCAACTGCA
      INFORMATION FOR SEQ ID NO: 10 SEQUENCE CHARACTERISTICS: LENGTH: 1329 base pairs TYPE: mucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                    Conservative
                                                                                                                                                                    Best Local Similarity
Matches 572; Conserv
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US-10-114-104-108
                                                                                                                      US-08-979-847-108
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GENERAL INCOMENTATION:

APPLICANT: Jacobs, John M.

APPLICANT: Lowaline, Edward R.

APPLICANT: Colling. Racie, Lisa A.

APPLICANT: Evans, Cheryl

APPLICANT: Evans, Cheryl

APPLICANT: Bowman, Michael R.

APPLICANT: Spanlding, Vikki

APPLICANT: Spanlding, Vikki

APPLICANT: Carlin-Duckett, McKeough

APPLICANT: Genetics Institute, Inc.

APPLICANT: Genetics Institute, Inc.

APPLICANT: Genetics 10000-10A

CURRENT FILING DATE: 2002-04-02

EARLIER APPLICATION NUMBER: 09/413,232

EARLIER FILING DATE: 1999-10-06

NUMBER OF SEQ ID NOS: 321

SEQ ID NO 134

LIBRITH: 2946
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                                                                 19991 ACTABABATGCTBATTAGGCBABABCBGGBGGTBABGBABATAGCCBATCACCTTTTGCCTG
                                                                                                   481 AGAGCACAGGGGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
                                   ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
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                                                                                                                                                                       541 CAACCCCCTTTGGGTCCCCTTTGTATGGGCGCTCTGTTTTCACTCTATT
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Best Local Similarity 91.5%; Pred. No. 1.9e-155;
Matches 581; Conservative 0; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                          ; Sequence 134, Application US/10114893; Publication No. US20020193567A1; GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-10-114-893-134
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            677 ACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCCAATCATCTATTGCCTG 736
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                                                                                                                1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA
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                                                                       0; Gaps
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Best Local Similarity 94.8%; Pred. No. 5e-158;
Matches 562; Conservative 0; Mismatches 31; Indels 0;
                                                                                                                                                                                                                                                                                            Sequence 910, Application US/10087192
| Sequence 910, Application US/10087192
| Publication No. US2002018286A1
| GENERAL INFORMATION:
| APPLICANT: Morris, David W. |
| APPLICANT: Morris, David W. |
| TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CURRENT FELING DATE: 2002-03-01
| FILE REFERENCE: 2204-03-01
| CURRENT FAPLICATION NUMBER: US 09/747,377
| PRIOR FILING DATE: 2001-12-22
| PRIOR FILING DATE: 2001-03-02
| NUMBER OF SEQ ID NOS: 2059
| SOFTWARE: FRAESEQ for Windows Version 4.0
| LENGTH: 21646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(21646)
CTHER INFORMATION: n = A,T,C or G
US-10-087-192-910
                                                                                                                                                                                        601 ATTAAATCTTGCAACTGAA 619
                                                                                                                                                                                                                   857 ATTAAATCATGCAACTGCA 875
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ORGANISM: Homo sapiens
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US-10-087-192-910
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Sequence 3, Application US/09731231A

Sequence 3, Application US/09731231A

Patent No. US20020082189A1

GENERAL INFORMATION:

APPLICANT: GUEGLER, Karl et al

APPLICANT: GUEGLER, Karl et al

TITLE OF INVENTION: ACID MULECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/09/731,231A

CURRENT FILING DATE: 2000-12-07

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 326014
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                                                              1671 ACATCCACCTTTAAACACGGGGCTTGCAACTTAGCTCACACCTGACCAATCAGGGGGCTC
                                                                                                              1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTAAAACTA
                                                                                                  ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
                                                                                                                                                    481 AGAGCACAGCGGGAGGGACAAGGATCGGGATATAAACCCCAGGCATTCGAGCCGGCAACGG
                                               361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGGTC
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83.9%; Score 532.8; DB 9;
Best Local Similarity 90.5%; Pred. No. 3.6e-154;
Matches 583; Conservative 0; Mismatches 52;
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; OTHER INFORMATION: n = A,T,C or
US-09-731-231A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Human
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                 ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
                                                                 481 AGAGCACAGCGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
                                                                                                                                                        CAACCCCCTTTGGGTCCCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCACTCT
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  GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGGTTC
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                                                                                                                                                                                                                                      2911 ATTAAATCTTGCAACTGCAAAAAAAAAAAAAAAA 2945
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Pred. No. 1.9e-155;
0; Mismatches 42;
                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/10016249 Publication No. US20030100053A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 91.5%;
Matches 581; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-016-249-3
                                                                                                                                                                                                                                                                                           US-10-016-249-3
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; Sequence 25, Application US/20040048298A1
; Sequence 25, Application No. US2004004829BA1
; GENERAL INFORMATION:
APPLICANT: PARAMHOS: BACCALA, Glaucia
APPLICANT: MALLET, Francois
APPLICANT: WOISET, Cecile
TITLE OF INVENTION: ENDOGRNEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN TITLE OF INVENTION: ENDOGRNEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN TITLE OF INVENTION: ENDOGRNEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN TITLE OF INVENTION: WOMBER: US/10/632,793
CURRENT APPLICATION NUMBER: US/09/869,927
PRIOR FILING DATE: 2001-0-2
PRIOR FILING DATE: 2001-0-2
; PRIOR FILING DATE: 2001-0-12
; PRIOR APPLICATION NUMBER: FR 99/00888
PRIOR APPLICATION NUMBER: FR 99/00888
; SOFTHARE: PATENTING DATE: 1999-01-21
; NUMBER OF SEQ ID NOS: 33
; SOFTHARE: PATENTIN VERSION 3.1
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                                                                                     GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATC-----
                                                                                                                                                                                        412 AGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Homo sapiens
US-10-632-793-25
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US-10-632-793-25
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                                                                                                                                Sequence 3, Application US/10751985;
Publication No. US20040126861A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
ACTUAL OF INVENTION:
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROFEINS, AND USES;
TITLE OF INVENTION: THEREOF;
TITLE REPREBLUCE: CLOO1007CON
CURRENT FILING DATE: 2004-01-07;
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FRASE PRACE OF Windows Version 4.0
SEQ ID NO 3
SEQ ID NO 3
SEQ ID NO 3
SEQ ID NO 3
SEQ ID NO 3
SEQ ID NO 3
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                                TATTGCCTGAGAGCACAGCGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGC
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83.9%; Score 532.8; DB 18;
Best Local Similarity 90.5%; Pred. No. 3.6e-154;
Matches 583; Conservative 0; Mismatches 52;
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LOCATION: (1)...(326014)
OTHER INFORMATION: n = A,T,C or G
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US-10-751-985-3/c
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NAME/KEY: misc feature
LOCATION: (1). T. (283351)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
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Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO101499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT PILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17995
LENGTH: 283351
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                                                                                                                            GATGGAGTCCATGACTAAGATCCACCGTGGACCCCTGGACCGGCCTGCTAGCCCATGCTC
                                                                               CTAAGAATCCCTAAGCCTAGCTGGGAAGGTGACCGCATCCACCTTTAAACACGGGGCTTG
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                                                          CGAAGAATCCCTAAGCCTAGCTGGAAGGTGACTGCATCCACCTCTAAACATGGGGCTTG
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; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-719-993-7065
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                              CGTCGGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGATGGGGGACTGAGAGAC
                                                                               AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
                                                                                                  361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGGGGTC
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Publication No. US20040265849A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASS
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASS
TITLE REFERENCE: CLOO1496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
CURBEN FILING DATE: S4342
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches 568; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 283351
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(see Tables 1-
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US-10-741-600-17676

US-10-741-600-17676

Sequence 17676, Application US/10741600

Publication No. US20050026169A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE REFERENCE: CLO01499

TITLE REFERENCE: CLO01499

CURRENT APPLICANION NUMBER: US/10/741,600

CURRENT APPLICANION NUMBER: US/10/741,600

CURRENT PILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 176706
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                                                                                                                                                                                              GTTTGTCTTCAAAATCAAAACTGTAAAACTACAAATTGTTCTTCAAATGGAGCACCA
                                                                                                                      447 GGAGGTAAAGAAATAGCCAATCATCTATTGCCTGAGAGCACAGCGGAGGGACAAGGATC
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            CGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACTGCATCCACCT
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Pred. No. 1.1e-150;
1; Mismatches 33; 1
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| LOCATION: (11)...(1980090)
| OTHER INFORMATION: n = A,T,C or G,
US-10-741-600-17676
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93.4%;
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Best Local Similarity 93.4
Matches 568; Conservative
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                                                                                    CAACTTAGCTCACACCCGACCAATCAGAGGCTCACTAAAATGCTAATTAGGCAAAAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: GRNETIC POLYMORPHISMS ASS
TITLE OF INVENTION: GRNETIC POLYMORPHISMS ASS
TITLE OF INVENTION: ALZHEIMER'S DISEASE, ME'
FILE REPERBNCE: CL001496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT APPLICATION NUMBER: US/10/719,993
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FASTSEQ FOR WINGOWS Version 4.0
SEQ ID NO 6815
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6815, Application US/10719993 Publication No. US20040265849A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (1)...(1980090)
OTHER INFORMATION: n = A,T,C or G,
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US-10-719-993-6815
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                                                                                   2446 AGGACTAGCTGGATTCCTAGGCTGACTAAGAATCCTTAAGCCTAGGTGGGAAGGTGACC
                                                                                                                                                                                                                                                                                                       481 AGAGCACAGCGGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
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                                                              AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGGTGGAAGGTGACT
                                                                                                                                           361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
                                                                                                                                                                                                                        ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/10133036
; Beduence 1, Application US/10133036
; Publication No. US20040054133A1
; GENERAL INFORMATION:
; APPLICANT: Conrad, Bernard
; TITLE OF INVENTION: Multiple Sclerosis-Related Superantigen
; FILE REPRENCE: 23135-507
; CURRENT APPLICATION NUMBER: US/10/133,036
; CURRENT FILING DATE: 2002-04-26
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE PELICATION VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 82.0%; Score 521; DB 17; Length 2782; Best Local Similarity 90.2%; Pred. No. 1.9e-151; Matches 573; Conservative 0; Mismatches 50; Indels 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2746 ATTABATCTTGCAACTGCAAAAAAAAAAAAAAA 2780
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; ORGANISM: Human endogenous retrovirus
US-10-133-036-1
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APPLICANT: PARAPHOS-BACCALA, Glaucia
APPLICANT: PARAPHOS-BACCALA, Glaucia
APPLICANT: WOISSET: Cecile
TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGWENT ASSOCIATED WITH AN
TITLE OF INVENTION: BUDGENEOUS NUCLEIC ACID FRAGWENT ASSOCIATED WITH AN
TITLE OF INVENTION: AUTOIMMUNE DISBASE, LABELING METHOD AND REAGENT
FILE REFERENCE: 110048
CURRENT APPLICATION NUMBER: US/09/869,927
PRIOR APPLICATION NUMBER: US/09/869,927
PRIOR APPLICATION NUMBER: ET/FR00/00144
PRIOR APPLICATION NUMBER: FR 99/00888
PRIOR PILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: FR 99/00888
PRIOR RELING DATE: 1999-01-21
PRIOR PILING DATE: 1999-01-21
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PACENTIN VETSION 3.1
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                                                                                         CAACTTAGCTCACACCGACCAATCAGAGAGCTCACTAAAATGCTAATTAGGCAAAAATA
                                                                                                                                                                      Gaps
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Pred. No. 5.9e-152;
0; Mismatches 49; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 26, Application US/10632793; Publication No. US20040048298A1; GENERAL INFORMATION:
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1777677 AAAAAAA 1777684
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Matches 574; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-632-793-26
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APPLICANT: Soppet, Daniel
APPLICANT: Soppet, Daniel
APPLICANT: Soppet, Daniel
APPLICANT: Endress, Gregory
APPLICANT: Endress, Gregory
APPLICANT: Endress, Gregory
APPLICANT: Ener; Reinhard
APPLICANT: Carter, Kenneth
ITILE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
ITILE OF INVENTION: Cancer Gene Sets
ITILE OF INVENTION: Cancer Gene Sets
FILE REFERENCE: 68929-64
CURRENT FILING DATE: 2003-04-29
CURRENT FILING DATE: 2000-09-29
PRIOR PELLOR DATE: 2000-09-29
PRIOR APPLICATION NUMBER: U.S. 60/236,842
PRIOR PELLING DATE: 2000-11-01
PRIOR PELLING DATE: 2000-11-01
PRIOR PELLING DATE: 2000-11-01
PRIOR PELLING DATE: 2000-11-01
SEQ ID NOS: 1067
SEQ ID NO 81
LEAGTH: 56093
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                                                                     301 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
                                                                                               361 GCATCCACCTCTAAACATGGGGGCTTGCAACTTAGCTCACACCAGACCAATCAGAGAGCTC
                                                                                                                                                                                   ACTAMANTGCTANTTAGGCAMANTAGGAGGTANAGAMATAGCCANTCATCTTGCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 81, Application US/09873367C; Publication No. US20030165839A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
US-09-873-367C-81
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APPLICANT: Soppet, Day
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US-09-873-367C-81
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paquence 1, Application US/09902535

patent No. US20020102330A1

GENERAL INFORMATION:

APPLICANT: Keith, Jr., James C.

APPLICANT: Mi. Sha

TITLE OF INVENTION: Methods and compositions for diagnosing

TITLE OF INVENTION: and treating preeclampsia and gestational trophoblast

TITLE OF INVENTION: disorders

TITLE OF INVENTION: disorders

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                                                                                                                                         421 ACTABARTGCTARITAGGCARARATAGGAGGTARAGARATAGCCARCATCTATTGCCTG
                                                                                                                                                                                                                             2566 ACTAMAATGCTAATTAGGCAAAGACAGGAGGTAAAGAAATAGCCAATCATTATTGCCTG
                                                                                                                                                                                                                                                                                          AGAGCACAGGGGGAGGACAAGGATCGGGGATATAAACCCCAGGCATTCGAGCCGGCAACGG
                                                                                                           361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
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                              AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTAAATCTTGCAACTGCAAAAAAAAAAAAAAAA 2780
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Best Local Similarity 91.4%; Pred. No. 2.5e-150;
Matches 564; Conservative 0; Mismatches 41;
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; NAME/KEY: CDS
; LOCATION: (930) ... (2546)
US-09-902-535-1
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US-09-902-535-1
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LOCATION: (2398)..(2398)
OTHER INFORMATION: n = a or g or
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LOCATION: (3787)..(3787)
OTHER INFORMATION: n = a or
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NAME/KEY: misc feature
LOCATION: (4115)..(4115)
COTHER INFORMATION: n = a or
FEATURE:
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NAME/KEY: misc feature
LOCATION: (2213)..(2213)
OTHER INFORMATION: n = a or
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                NAME/KEY: misc_feature
LOCATION: (1309)..(1309)
OTHER INFORMATION: n = a
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NAME/KEY: misc_feature
LOCATION: (1331)..(1331)
OTHER INFORMATION: n = a
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Best Local Similarity
Matches 552; Conservat
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Sequence 30, Application US/10632793

Sequence 30, Application US/10632793

Sequence 30, Application No. U3200400482981

GENERAL INFORMATION:
APPLICANT: MALLET, Francois

APPLICANT: WOISSET, Cecile

TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN TITLE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT

FILE OF INVENTION: AUTOIMUNE 105/09/869,927

PRIOR PELING DATE: 2001-10-22

PRIOR APPLICATION NUMBER: PCT/FR00/00144

PRIOR FILING DATE: 2000-01-21

PRIOR FILING DATE: 1999-01-21

NUMBER OF SEQ ID NOS: 33

SOFTWARE PATENTION NUMBER: FR 99/00888

SOFTWARE PATENTION NUMBER: PCT/FR00/0144

SOFTWARE PATENTION NUMBER: PCT/FR00/0144

SOFTWARE PATENTION NUMBER: PCT/FR00/0144

PRIOR FILING DATE: 1999-01-21

SOFTWARE PATENTION NUMBER: PCT/FR00/0144

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CTGGACCGGCCTGCTAGCCCACGATCTGATGTTAATGACATCAAAGGCACCCCTCCTGAG 37441
                                                                                       37442 GAAATCTCAGCTGCACAACCTCTACTACGCCCCAATTCAGCAGGAAGCAGTTAGAGCGT 37501
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LOCATION: (355)..(355)
OTHER INFORMATION: n = a or g or
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LOCATION: (307)..(307)
OTHER INFORMATION: n = a or
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NAME/KEY: misc_feature
LOCATION: (198)..(198)
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                       241 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC
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COCCARCOCCARCOCCCTTTGGGTCCCCTTTGTATGGGCGCTCTGTTTTCACTCTA
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Rest Local Similarity 89.3%; Pred. No. 3.3e-144;
Matches 577; Conservative 0; Mismatches 57; Indels
                                                                                                     630
                                                                                                                                                                                         Sequence 1666, Application US/10087192
Sequence 1666, Application US/10087192
Sequence 1666, Application US/10087192
Sequence 1666, Application US/10087192
Sequence 1666, Application US/2002018286A1
GENERAL INFORMATION:
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER.
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ 1D NOS: 2059
NUMBER OF SEQ 1D NOS: 2059
SOFTWARE: FRELSEQ for Windows Version 4.0
                                                                             NAME/KEY: misc_feature

LOCATION: (1)...(285020)

OTHER INFORMATION: n = A,T,C or G

US-10-087-192-1666
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LENGTH: 285020
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80.4%; Score 510.6; DB 13; Length 161334;
Best Local Similarity 90.0%; Pred. No. 2.2e-147;
Matches 575; Conservative 0; Mismatches 49; Indels 15; G
                                                                                                             US-10-087-192-730/C
US-10-087-192-730/C
US-10-087-192-730/C
Sequence 730, Application US/10087192
Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: MOTIS, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT FILING DATE: 2002-03-01
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR PLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/7798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 730
LENGTH: LAND HALLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature

LOCATION: (1)...(161334)

OTHER INFORMATION: n = A,T,C or G

US-10-087-192-730
                                   601 ATTAAATCTTGCAACTG
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Sequence 28, Application US/10632793

Sequence 28, Application No. US20040048298A1

Sequence 28, Application No. US20040048298A1

GENERAL INFORMATION:

APPLICANT: PARANHOS-BACCALA, Glaucia

APPLICANT: WALLET, Francois

APPLICANT: VOISSET, Cecile

TITLE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT

FILE REPERENCE: 1100 NUMBER: US/10/632,793

CURRENT APPLICATION NUMBER: US/10/632,793
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D IN HEL100, SIGNAL = 6

D IN HEART, SIGNAL = 5.4

D IN BH474, SIGNAL = 5.9

D IN FETAL LIVER, SIGNAL = 6.7

D IN BRAIN, SIGNAL = 6.7

D IN BRAIN, SIGNAL = 6.3

D IN BONE MARROW, SIGNAL = 6.3

D IN LUNG, SIGNAL = 6.3

D IN LUNG, SIGNAL = 3.9
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Best Local Similarity 88.7%; Pred. No. 7.5e-145;
Matches 571; Conservative 0; Mismatches 54; Indels
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**APPLICANT. THAREAL DAVIA K.

**APPLICANT. THAREAL DAVIA K.

**APPLICANT. CHEM, WHENBERD B.

**TITLE OF INVENTION: CREW EXPRESSION ANALYSIS BY WICKOARRAY.

**CURRENT TAPLICANTON: CREW EXPRESSION ANALYSIS BY WICKOARRAY.

**CURRENT TAPLICANTON NUMBER: US 60/180, 312

**PRIOR FILLE OF INVENTION: CREW EXPLORATION NUMBER: US 60/180, 312

**PRIOR FILLE OF INVENTION: DOUG 00-34

**CURRENT TAPLICANTON NUMBER: US 60/20, 456

**PRIOR APPLICANTON NUMBER: PCT/USO1/0669

**PRIOR FILLING DATE: 2001-01-9

**PRIOR PLICATION NUMBER: PCT/USO1/0669

**PRIOR PLICATION NUMBER: PCT/USO1/0669

**PRIOR FILLING DATE: 2001-01-9

**PRIOR FILLING DATE: 2001-
                                                                                                                                                                                                                                 280084
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                                                                                  279966 TCTATCGCCTGAGAGCAC-GAGGGAGGGACAATGATCAGGATATAAACCCAGGCATTCAA
                                                                                                                                                                                                             TCTATTGCCTGAGAGCACAGGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGA
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ORGANISM: Homo sapiens
PEATURE:
OTHER INFORMATION: MAP TO AC002146.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL =
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                                                                                                                                                                                                                                                                                                                      CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
                                                                                                                                                                                                                                                          CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
                                                                                                                                                                                                                                                                          1053 CACATCGTTCTTCAAATGGAGCCCCAGATGCAGTCCATGACTAAGATCTACGCGGAATCC
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US-09-997-722-148
US-09-997-722-148

Sequence 148, Application US/09997722

Sequence 148, Application US/09997722

Sequence 148, Application Vo. US20040072154A1

Sequence 148, Application No. US20040072154A1

GENERAL INFORMATION:

APPLICANT: Engelhard, Eric

TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER

FILE REPERRNCE: A-71171/RMS/DCF;

CURRENT APPLICATION NUMBER: US/09/997,722

CURRENT FILING DATE: 2001-11-30

PRIOR PILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US/09/798,586

PRIOR FILING DATE: 2001-03-02
                                                                                                                                                                  10;
                                                                                                                                   Length 2052;
                                                                                                                                                                  Indels
                                                                                                                                      DB 17;
                                                                                                                                   77.7%; Score 493.2; DB 17
ilarity 91.2%; Pred. No. 7.7e-143;
Conservative 0; Mismatches 43;
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: Custom
SEQ ID NO 678
                                                                               TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                       Local Similarity
nes 549; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TT 1593
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Sequence 678, Application US/10276774
Publication No. US20040053245A1
Publication No. US20040053245A1
APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: No. US20040053245A1e1 Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
CURRENT FILING DATE: 2002-11-18
PRIOR PPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR PLICATION NUMBER: 09/496,914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       490 CGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGGCAACCCCT
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                                                                                                                                                                                                                                                                                    70 CTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCCGT
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0
                                                                                                                                                                                                                       Length 3372;
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                                                                                                                                                                                                                         Score 495.6; DB 17;
Pred. No. 1.7e-143;
0; Mismatches 44;
      PRIOR APPLICATION NUMBER: US/09/869,927
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: PCT/FR00/00144
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 1999-01-21
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 28
LENGTH: 3372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3342 TGCAACTGCAAAAAAAAAAAAAAAA 3367
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                                                                                                                                                                                                                           Query Match
Best Local Similarity 92.2%;
Matches 522; Conservative
                                                                                                                                                                TYPE: DNA; ORGANISM: Homo sapiens
US-10-632-793-28
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60/184,770; 60/184,774
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NAMEKKEY: misc_feature
1 O'THER INFORMATION: Incyte ID No. US20040048253A1 LG:429446.1:2000FEB18
US-10-220-120-15
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                                                                                                                                                                                                                                                                                                                                              APPLICANT: HODGSON, David M.
APPLICANT: HODGSON, David M.
APPLICANT: LINCOLN, Steath B.
APPLICANT: JACKSON, Stuart
ITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PT-1113 PCT
CURRENT APPLICATION NUMBER: US/10/220,120
CURRENT FILING DATE: 2002-08-26
                                                                                                                                                                                               ĸ.
                                                                                                                                                             ROSEN, Bruce H.
RUSSO, Frank D.
STOCKDREHER, Theresa
                                                          FONG, Willy T.
GREENAWALT, Lila B.
HILLMAN, Jennifer L
JONES, Anissa L.
                                                                                                                                                                                                                           MRIGHT, Rachel J.
YAP, Pierre E.
YU, Jimmy Y.
BRADLEY, Diana L.
BRATCHER, Shawn R.
DAM, Tam C.
DANIELS, Susan E.
DUFOUR, Gerard E.
FLORES, Vincent
                                                                                                                               LIU, Tommy F.
ROSEBERRY, Ann M.
                                                                                                                                                                                                                                                                                                               CHEN, Wensheng
COHEN, Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                DAFFO, Abel
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Best Local
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APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                       180 GGAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGAAGCAGTTAGAGCGG
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                                                                                                                                                                                                   1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAACTA
                                                                                                                                   DB 11; Length 22436;
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                                                                                                                                 Score 482.6; DB 11
Pred. No. 4.8e-139;
0; Mismatches 69;
                                                                                                                                 76.0%;
87.6%;
   NUMBER OF SEQ ID NOS: 301
SOFTWARE: PatentIn version 3.1
                                                                                                                                   Query Match
Best Local Similarity 87.65
Matches 565; Conservative
                                                                   TYPE: DNA
CORGANISM: Homo sapiens
US-09-997-722-148
                                  SEQ ID NO 148
LENGTH: 22436
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                                                                                                                                                                                                                                                               27 GTTTGTCTTCCAGAATCAAAACTGTAAAACTACAAATTGTTCTTCAAATGGAGCACCA
                                                                                                                         GATGGAGTCCATGACTAAGATCCACGGTGGACCCCTGGACCGGCCTGCTAGCCCATGCTC
                                                                                                                                                    181 GATGCAGTCTATGACTAAGATCTACCACAGACCCTTGGACCGGCCTGCTAGCCCATGCTC
                               Gaps
75.8%; Score 481.4; DB 17; Length
89.1%; Pred. No. 2.5e-139;
tive 0; Mismatches 56; Indels
                                   Matches 534; Conservative
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Sequence 15, Application US/10220120 Publication No. US20040048253A1 GENERAL INFORMATION:

RESULT 29 US-10-220-120-15

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8

APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: PANZER, SCOLT R.
APPLICANT: SPIRO, Peter A.
APPLICANT: SHAW, Purvi
APPLICANT: CHALUP, Michael S.
APPLICANT: CHALUP, Michael S.
APPLICANT: CHRNG, Simon C.
APPLICANT: CHRNG, Simon C.
APPLICANT: CHRNG, Steen A.
APPLICANT: D'SS, Steen A.
APPLICANT: AMSHEY, Stefan
APPLICANT: DAHL, Christopher R.

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1856 GGGGGGGACAATGATCAGGATATAAACTCAGGCATTCAAGCCAGCAATGGCTACCCACT 1915
                                                                                                                                                                             TIGGGICCCCCCCCTTTGIAIGGCGCTCTGTTTTCACTCTATITCACTCTATIAAAICT 609
                                                     430 CTAATTAGGGAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTGAGAGCACAG
                                                                                                          490 cgggaggagachaggarrgragarrarhanacccaggcarrcgagccagchacggchaccccrr
379 GGGGCTTGCAACTTAGCTCACACCCGACCAATC-----AGAGAGCTCACTAAAATG
                                                                                                                                                                                                                                                  610 TGCAACTGAAAAAAAAAAAAAAAA 635
                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/10204887; Publication No. US20030124569A1; GENERAL INFORMATION: APPLICANT: INCYTE GENOMICS, INC. APPLICANT: PANZER, SCOLT R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROSEN, Bruce H.
RUSSO, Frank D.
STOCKDREHER, Theresa K.
                                                                                                                                                                                                                                                                                                                                                                       PANZER, SCOTT R.
SPIRO, Peter A.
BANVILLE, Steven C.
SHAH, Purvi
CHALUP, Michael S.
CHRNG, Simon C.
CHEN, Alice
D'SA, Steven A.
ANGHEY, Stefan
DAHL, Christopher R.
DAM, Tam C.
DANIELS, Susan B.
DICOUR, Gerard E.
FLORES, Vincent
FONG, Willy T.
GREENAMALT, Lila B.
HILLMAN, Jennifer L.
JONES, Anissa L.
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ROSEBERRY, Ann M.
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LENGTH: 1564
TYPE: DNA
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1497 CCA-GCTCCCACATTAATGACATCAAAGGCACCCCTCCCGAGGAAATCTCAACTGCATGA 1555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 ACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGTCTGAGAGACAGGACTAGCTGGATTTCC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAGGCCAACGAAGAATCCCTAAGCCTAGCTGGAAGGTGACTGCATCCACCTCTAAACAT 378
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                                                                                                                                                                                                                                                     CGAAGAATCCCTAAGCCTAGCTGGAAGGTGACTGCATCCACCTCTAAACATGGGGCTTG 386
                                                                                                                      387 CAACTTAGCTCACACCCGACCAATCA-----GAGAGCTCACTAAAATGCTAATTAG 437
                                                                                                                                       GCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTGAGAGCACAGGGGGAGGG 497
                                                                                                                                                                                           498 ACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGGCAACCCCTTTGGGTCC 557
                                                                                  558 CCTCCTITGIAIGGCGCTCTGITTCACTCTAITTCACTCTATIAAATCTIGCAACT 616
                                                                                                                                                                                                                                                                                                               661 cerecertrichardedaderererritrearderarritraangrerrigeaaereeaeaer 719
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                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: HELIX RESEARCH INSTITUTE
APPLICANT: HELIX RESEARCH INSTITUTE
FILE OF INVENTION: No. US20030236392A1e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1148
LENGTH: 2349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 86.4%; Pred. No. 2.5e-134;
Matches 541; Conservative 0; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1148, Application US/10104047 publication No. US20030236392A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-10-104-047-1148
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                                                                    ROSEN, Bruce H.
RUSSO, Frank D.
STOCKDREHER, Theresa
                                                                                                                                       WRIGHT, Rachel J.
YAP, Pierre E.
YU, Jimmy Y.
BRADLEY, Diana L.
BRATCHER, Shawn R.
CHEN, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Incyte ID
HILLMAN, Jennifer
                                Tommy F.
SERRY, Ann M.
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                                                     ROSEBERRY
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                                                                                                                                                                                                                                                                                            GAATTGAAACTGTAAAACTACAAATGGTTCATCAAATGGAGCCCCAGATGCAGTCCATGA 1081
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                                                                                                                                                                                                                                                           GAATCAAAACTGTAAAACTACAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRGANISM: Homo sapiens
FRATURE:
NAME/KEY: misc_feature
CTHER INFORMATION: Incyte ID No. US20030124569A1 LI:813218.1:2000FEB01
FRATURE:
NAME/KEY: unsure
LOCATION: 307, 317-318, 335, 918, 921, 943, 1011
COTHER INFORMATION: a, t, c, g, or other
US-10-204-887-10
                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                 Score 449; DB 15;
Pred. No. 4.2e-129;
0; Mismatches 45;
                                                                                                                                                                                 Query Match
Best Local Similarity 90.9%;
Matches 490; Conservative C
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Sequence 17, Application US/10220120 Publication No. US20040048253A1 GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
                                                                                                                                                 CHEN, Alice
D'SA, Steven A.
AMSHEY, Stefan
DAHL, Christopher R.
DANIELS, Susan E.
DUFOUR, Gerard E.
                                                          PANZER, SCOTT R.
SPIRO, Peter A.
BANVILLE, Steven C.
SHAH, Purvi
CHALUP, Michael S.
CHANG, Simon C.
                                                                                                                                                                                                                                                        FLORES, Vincent
FONG, Willy T.
GREENAWALT, Lila B.
                                                          APPLICANT:
APPLICANT:
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GGGGACTGAGAGACTAGCTGGATTTCCTAGGCCAAGAAGATCCCTAAGCCTAG 346

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60/184,770; 60/184,774
APPLICANT: UCDEM, HOWAGON D.

APPLICANT: HODGSON, David M.

APPLICANT: LINCOLN, Stephen E.

TILLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT PILID DATE: 2002-08-26

CURRENT FILLING DATE: 2002-08-26

CURRENT FILLING DATE: 2002-08-26

CONRENT FILLING DATE: 2002-08-26

GO/184, 703; GO/184, 771; GO/184, 773; GO/184, 776; GO/184, 776; GO/184, 777; GO/184, 777; GO/184, 777; GO/184, 777; GO/184, 777; GO/184, 777; GO/184, 777; GO/184, 777; GO/184, 777; GO/184, 877; GO/184, 877; GO/184, 777; GO/184, 777; GO/184, 877; GO/184, 777; GO/185, 216; GO/204, 921; GO/204, 921; GO/204, 921; GO/204, 921; GO/205, 221; GO/205, 221; GO/205, 221; GO/205, 221; GO/205, 224; CO/205, 224; CO/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCACCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGGAA 226
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nilarity 90.3%;
Conservative 0
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502; Conserv
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; LOCATION: 120, 765
; OTHER INFORMATION:
US-10-220-120-17
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Best Local S:
Matches 502
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                                                                                       6828
                                                                                                                                               301 AGGACTAGCTGGATTTCCTAGGCCAACGAATCCCTAAGCCTAGCTGGG-AAGGTGAC 359
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-----AGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAG
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APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 522452001000
CURRENT APPLICATION NUMBER: US/10/322,281
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54;
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Pred. No. 9.7e-122;
0; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 718, Application US/10322281; Publication No. US20040126762A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1) ... (44063)
; OTHER INFORMATION: n = A, T, C or G
US-10-322-281-718
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86.1%;
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Best Local Similarity 86.1
Matches 556; Conservative
                                                                                                                                                                                                                                                                                                                                              582 TTTCACTCTATT 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
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US-10-322-281-718
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                                                                              301 CTGGGAAGGTGACCGCGTCTACCTTTAAACACGGGGCTTGCAACTTAGCTCACACCCAAC 360
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           GGGGACTGAGAGAGAGTAGCTGGATTTCCTAGGCTGACTAAGAATCCCTAAGCCTAG 300
                                                                                                                        457
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Sequence 9936, Application US/2003009974A1

GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Lillie, James
APPLICANT: Lillie, James
APPLICANT: Lillie, James
APPLICANT: MI, Yongyao
APPLICANT: MI, Yongyao
APPLICANT: MI, Yongyao
APPLICANT: MI, Yongyao
APPLICANT: MI, Yongyao
APPLICANT: MI, Yongyao
APPLICANT: MI, Yongyao
APPLICANTON: PREVENTION: PREVENTION AND TITLE OF INVENTION: PREVENTION OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT PELICATION NUMBER: 60/306,220
PRIOR FILLING DATE: 2002-07-18
MUMBER OF SEQ ID NOS: 14084
NUMBER OF SEQ ID NOS: 14084
SOSTWARE FRAESE FRAESEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGAC-TAAGATCCACCGTGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTGGACCGGCCTGCTAGCCCCATGCTCGATGATGACATTGAAGGCACCCCTCCCGA
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                                                                                                                                                 AATAGCCAATCATCTTGCCTGAGAGCACAGGGAGGAACAAGGATCGGGATATAAAC
                                                                                                                                                                                                                                                                                 407 CAATC-----AGAGGGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGA
                                                                                                                                                                                                                                                                19; Gaps
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68.4%; Score 434.4; DB 14; Length 7974;
Best Local Similarity 87.7%; Pred. No. 3.3e-124;
Matches 537; Conservative 0; Mismatches 56; Indels 19;
                                                                                                                                                                                                                                                                                                                                                           CTGTTTTCACTCTATT 556
                                                                                                                                                                                                                                                                                                                                         CTGTTTTCACTCTATT 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-198-846-9936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 9936
LENGTH: 7974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
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                                                                                                                                                                                                                                                                                                                                                                                422 AGCCAGCAATRGCTACCCTCTATGGATCCCCTCTTTGTATGGAGGCTCTGTCTTCACT 481
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US-10-027-632-289680

Sequence 289660, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Dolymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: 2022-04-30

PRIOR APPLICATION NUMBER: US 60/128,006
PRIOR APPLICATION NUMBER: US 60/128,006
PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1209-10-24

PRIOR FILING DATE: 1299-10-24

PRIOR FILING DATE: 1999-10-24

PRIOR FILING DATE: 1999-10-26

PRIOR FILING DATE: 1999-10-26

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PRIOR FILING DATE: 1999-10-26

PRIOR FILING DATE: 1999-10-26

PRIOR FILING DATE: 1999-10-26

PRIOR FILING DATE: 1999-10-26

PRIOR FILING DATE: 1999-10-26

PRIOR FILING DATE: 1999-10-30

PRIOR FILING DATE: 1999-10-26

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                                                                                                                                  242 GGGAAGGTGACTGCATCCACCTTTAAACACGGGGCTTGCAACTTAGCTCACGCCGACCA
                                                                                                                                                                                                                                           302 ATAAGAGAGCTTACTAAAATGCTAATTAGGCAAAAACAGGAGGTAAAGAAATAGCCAATC
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182 GGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCCAACTAAGAATCCCTAAGCCTAGGT
                                                                                                                                                                                                                                                                                                                                  ATCTATTGCCTGAGAGCACAGGGAGGGACAAAGATCGGGATATAAACCCAGGCATTCG
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93.4%; Pred. No. 1.1e-121;
iive 1; Mismatches 30;
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; ORGANISM: Human
US-10-027-632-289680
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Matches 453;
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                                                                                                                                                                                                                                  1492 TACATTGCCTGAGAGCACAGGGGAGGACAATGATCGGGATATAAACCCAGGCAATCGA 1551
               1312 AGGACTAACTGGATTTCCTAGGCCAACTAAGAATTCCCAAGCCTAGCTGGGAAAGGTGAC 1371
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                                                                                                                        APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Octymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT PELING DATE: 2002-04-30
FRIOR PELING DATE: 2002-04-30
FRIOR PELING DATE: 2000-07-12
FRIOR PELING DATE: 2000-04-20
FRIOR PILING DATE: 2000-04-20
FRIOR PELING DATE: 2000-04-20
FRIOR PELING DATE: 2000-04-24
FRIOR PELING DATE: 2000-03-24
FRIOR PELING DATE: 2000-02-4
FRIOR PELING DATE: 2000-02-4
FRIOR PELING DATE: 2000-02-4
FRIOR PELING DATE: 1999-11-23
FRIOR PELING DATE: 1999-11-23
FRIOR PELING DATE: 1999-09-28
FRIOR PELING DATE: 1999-09-28
FRIOR PELING DATE: 1999-09-28
FRIOR PELING DATE: 1999-09-28
FRIOR PELING DATE: 1999-09-28
FRIOR PELING DATE: 1999-08-09
FRIOR FILING DATE: 1909-08-09
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                                                                                                                                                                                                412 -AGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAG-CCAATCA
                                                                                                                                                                                                                                                                                                                  410 TCTATTGCCTGAGAGCACAGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGA
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                                                                                360 IGCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATC
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Pred. No. 1.1e-121;
1; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 289680, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
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Best Local Similarity 93.4%;
Matches 453; Conservative
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                                                                                                                                                                       479 TGAGAGGACGGGAGGGACAAGGATCGGGATATAAA-CCCAGGCATTCGAGCCGCAA 537
                                                                                                                                                                                                                                                                     538 cagcaacccccrrrragercccrrrcrrrararegecccrrrrrrrarares97
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APPLICAMY: INFORMATION: AS LEADER B.; ALTUS, Christina M.;
APPLICAMY: INFORMATION.
APPLICAMY: DINCOLM, Stephen B.; ALTUS, Christina M.;
APPLICAMY: DINCOLM, Stephen B.; ALTUS, Christina M.;
APPLICAMY: DONES, Anissa L.; DAM, Tam C.;
APPLICAMY: FLORES, Vincent Z.; DAFFO, Abe;
APPLICAMY: FLORES, Vincent Z.; DAFFO, Abe;
APPLICAMY: PLORES, Vincent Z.; DAFFO, Abe;
APPLICAMY: PERALTA, Careyna H.; DAVID, Marie H.;
APPLICAMY: LEWIS, Samantha A.
APPLICAMY: LEWIS, Samantha A.
APPLICAMY: LEWIS, Samantha A.
APPLICAMY: LEWIS, Samantha A.
APPLICAMY: LEWIS, Samantha A.
APPLICAMY: LEWIS, Samantha A.
APPLICAMY: LING DATE: 2003-07-15
CURRENT APPLICATION NUMBER: US 60/261,865
RRIOR FILING DATE: 2003-01-16
RRIOR FILING DATE: 2001-01-16
RRIOR FILING DATE: 2001-01-16
RRIOR FILING DATE: 2001-01-16
RRIOR APPLICATION NUMBER: US 60/263,329
RRIOR APPLICATION NUMBER: US 60/263,131
RRIOR APPLICATION NUMBER: US 60/263,131
RRIOR APPLICATION NUMBER: US 60/263,106
RRIOR RILING DATE: 2001-01-19
RRIOR APPLICATION NUMBER: US 60/263,063
RRIOR FILING DATE: 2001-01-19
RRIOR RILING DATE: 2001-01-19
RRIOR FILING DATE: 2001-01-19
RRIOR RILING DATE: 2001-01-19
RRIOR FILING DATE: 2001-01-19
RRIOR RILING DATE: 2001-01-19
RRIOR FILING DATE: 2001-01-17
RRIOR APPLICATION NUMBER: US 60/263,063
RRIOR RILING DATE: 2001-01-19
RRIOR RILING DATE: 2001-01-17
RRIOR APPLICATION NUMBER: US 60/263,063
RRIOR FILING DATE: 2001-01-17
RRIOR APPLICATION NUMBER: US 60/263,063
RRIOR FILING DATE: 2001-01-17
RRIOR APPLICATION NUMBER: US 60/263,063
RRIOR RILING DATE: 2001-01-17
RRIOR APPLICATION NUMBER: US 60/263,063
RRIOR RILING DATE: 2001-01-17
RRIOR APPLICATION NUMBER: US 60/263,063
RRIOR FILING DATE: 2001-01-17
RRIOR PILING DATE: 2001-01-17
RRIOR APPLICATION NUMBER: US 60/263,063
RRIOR FILING DATE: 2001-01-17
RRIOR PILING DATE: 2001-01-17
RRIOR PILING DATE: 2001-01-17
RRIOR PILING DATE: 20
                                                                         421 ACTAAAATGCTAATTAGGCAAAAA-TAGGAGGTAAAGAAAT-AGCCAATCATTTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: unsure
LOCATION: 484
OTHER INFORMATION: a, t, c, g, or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 47, Application US/10466531; Publication No. US20040166500A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Sequence 17699, Application US/10741600
Sequence 17699, Application US/2005026169A1
GENERAL INFORMATION:
APPLICANT CARGILL, Michele et al.
APPLICANT CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SEQ ID NO 17699
SEQ ID NO 17699
LENGTH: 50353
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                    GGACTGAGAGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCT
                                           182 GGACTGAGAGAGAGAGTAGCTGGATTTCCTAGGCCAACTAAGAATCCCTAAGGT
                                                                                                               349 GGGAAGGTGACTGCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCA
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Best Local Similarity 83.99
Matches 535; Conservative
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CONGANISM: Homo sapiens
US-10-741-600-17699
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                                                                                                                                                                  7;
                                                                                                                                 548;
EXPRESSED IN BONE MARROW, SIGNAL = 1.4
EST HUMAN HIT: BIO87886.1, EVALUE 1.00e-122
EST-HUMAN HIT: BIO87886.1, EVALUE 1.00e-122
SWIĞSPROT HIT: P03384, EVALUE 2.00e-01
NT HIT: AL163280.2, EVALUE 0.00e+00
                                                                                                                                 Length
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                                                                                                                                                                     Indels
                                                                                                                               62.3%; Score 395.8; DB 16;
.larity 89.5%; Pred. No. 1.1e-112;
Conservative 0; Mismatches 47;
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US-10-242-355-1175.
Sequence 1175. Application US/10242355
Publication No. US20030235831A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TTILE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFRENCE: PC003C1
CURRENT FILING DATE: 2002-09-13
PRIOR PELING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,897
PRIOR PELING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-08-14
PRIOR FILING DATE: 2000-06-11
PRIOR FILING DATE: 2000-06-11
PRIOR FILING DATE: 2000-06-11
PRIOR FILING DATE: 2000-06-11
PRIOR FILING DATE: 2000-06-11
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
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     ; OTHER INFORMATION: E:
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; OTHER INFORMATION: S:
; OTHER INFORMATION: SI
; OTHER INFORMATION: N
                                                                                                                                                      Best Local Similarity
Matches 461, Conser
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US-10-242-355-1175/c
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                                                                                                                                                                                                                                 ACATTGAAGGCACCCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTATGCCCCAATT
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                                                                                   Gaps
                                             Length 1394;
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OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.99
OTHER INFORMATION: EXPRESSED IN FITAL LIVER, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 6.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Renk, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUTTILE OF INVENTION: EXPRESSION ANALYSIS TWO FILE REFERENCE: AEOMICA-X-2 CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                             5; DB 18;
1.1e-118;
                                             Score 415.6; D
Pred. No. 1.1e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8554, Application US/10029386 Publication No. US20030194704A1 GENERAL INFORMATION:
                                             65.4%;
ilarity 90.8%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
                                           Query Match
Best Local Similarity
Matches 532; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 TCATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGGACTGAGAGA
                                                                                                                                                                                    Query Match 61.2%; Score 388.4; DB 17; Length 23855; Best Local Similarity 83.1%; Pred. No. 1.3e-109; Matches 552; Conservative 0; Mismatches 71; Indels 41; Gaps
                                                                 - See File Wrapper or PALM
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
PRIOR FILING DATE: 2000-08-14
PRIOR FILING DATE: 2000-07-14
Remaining Prior Application data removed - 8; SEQ ID NOS: 1267
SEQ ID NO 1175
LENGTH: 23855
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Job time : 365.955 secs
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CORGANISM: Homo sapiens
US-10-242-355-1175
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. scale c search, using sw model February 21, 2005, 06:52:54; Search time 1974.67 Seconds (without alignments) 12240.400 Million cell updates/sec 05-09-319-156B-6 635 1 ccctgtatctttaacctccttgaaaaaaaaaaaa	000000000	ch 0% ch 100% st 45 summaries ** ** **	r of results predicted by chance to have a equal to the score of the result being printed, yais of the total score distribution. SUMMARIES DE ID		1 AA781423 AA781423 aj26c03.8 5 BA439636 BA439636 BA439636 BA439636 BA439636 BA439636 BA439636 BA439636 BA439636 BA439636 BA439636 BA439636 BA439636 BA439636 BA33042 7 CN645411 ELLUMIGEN CN645411 ILLUMIGEN AG026287 Phono sapi AG033781 Phono sapi AG033781 Phono sapi AIS98135 EN14410.x BE1963185 BE1963185 E95710.x BE1963185 E95710.x BA380176 BA3
Copyright OM nucleic - nucleic search, Run on: February 21, Title: US-09-319-15 Perfect score: 635 Sequence: 1 cctgtatct Scoring table: IDENTITY_NUC Gapop 10.0 , Searched: 34239544 seq	Minimum DB seq length: 0 Maximum DB seq length: 2000	Post-processing: Minimum Mat Maximum Mat Listing fix Database : EST:* 1: 9D-est1: 2: 9D-est2: 3: 9D-htc:* 5: 9D-est2: 5: 9D-est2: 6: 9D-est5: 7: 9D-est5: 7: 9D-est5: 8: 9D-est5: 9: 9D-est6: 9: 9D-est6: 9: 9D-est6: 9: 9D-est6:	Pred. No. is the number score greater than or e and is derived by analy the second of the second score Match Length	498.8 77.6 4 498.8 77.6 4 488 76.9 6 485.6 76.9 7 47.6 5 7 47.6 5 10 466.6 73.8 11 454.6 73.2 11 454.6 73.2 12 453.6 71.4	437 68.8 435.4 68.8 430.2 67.7 430.2 67.7 423 66.8 415.8 66.6 397.4 62.6 397.4 62.6 395.2 62.2

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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 9100 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
191 910 910 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
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                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                     Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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/organism="Homo sapiens"
/mol type="mRNN"
/db_xref="taxon:9606"
/clone="CSOBOLL2Y124"
/tissue type="placenta"
/plasmid="pcMvSpoRT_6"
                                                                                                    Homo sapiens (human)
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  cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.E. Consortium/Link at: http://image.llnl.gov Series: IRAL Plate: 41 Row: m Column: 10 This clone has the following problem: retained intron. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTGAGAGCACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.6%; Score 498.8; DB 3;
.larity 92.6%; Pred. No. 3.6e-133;
Conservative 0; Mismatches 42;
                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
mol type="mRNM"
/db xref="texon:9606"
/clone="INAGE:4724433"
/clone="type="Placenta"
/clone_Tib="NIH MGC_79"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pDNR-LIB"
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) and the strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I, (bases I to 2500)
Li, W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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                                                                                                                                                        1 CCCGGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAACTGTAAAACTA
301 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
                               421 ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
                                                                                                                  361 GCATCCACTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
                                                                                                                                                                                                                                                                                                                                                                 AGAGCACAGGGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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/nol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSDD1051YM13"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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HTC; CNSLT CDNA.
Homo sapiens (human)
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Direct Submission
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
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                                                      2635 AGAGCACAGCAGGAGGACAATGATGATCGGGATATAAACCCAAGTCTTCGAGCCGGCAACGG
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         AGAGCACAGGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
                                                                                                                        CAACCCCTTTGGGTCCCTCCTTTGTATGGGCGCTCTGTTTCACTCTATTT 594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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Pred. No. 3.4e-130;
0; Mismatches 42;
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HTC; CNSLT CDNA.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 90.8%;
Matches 536; Conservative (
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full-length cDNA clone CSODIO44YKO6 of Placenta Cot 25-normalized of Homo sapiens (human).
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(Dases 1 to 2748)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                    259 CIGGACCGGCCTGCTAGCCCACGATCTGATGTTAATGACATCAAAGGCACCCCTCCTGAG
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                                                                                   15;
                                     Length
                                                                                   Indels
                                76.5%; Score 485.6; DB 4;
ilarity 89.9%; Pred. No. 2.2e-129;
Conservative 0; Mismatches 49;
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HTC; CNSLT CDNA.
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Homo sapiens
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Genoscope.
Direct Submission
                                                                 Best Local Similarity
Matches 570; Conserv
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                                             Query Match
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CR625046
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Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

B. (Dases I to 771)

I. (Dases I to 771)

I. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CLONG distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLAM11015 row: d column: 23

High quality sequence stop: 762.

Location/Qualifiers
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602852690F1 NIH_MGC_10 Homo Bapiens cDNA clone IMAGE:4993894 5',
mRNA sequence.
BIO87886
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CTGGACCGGCCTGCTAGCCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
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                                                                                             GAAATCTCAACTGCACAACCCCCTACTATGCCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
                                                                                                                      241 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGGACTGAGAGAC
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/tissue type="embryonic stem cell, retinoic acid and mitogen-treated hES cell line H7" /clone lib="GRN PRENKU" /note="oligo dT primed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic and mitogens."
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 719)

Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.

Transcriptome characterization elucidates signaling networks that
control human BS cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
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                                                                                                                                                    Geron Corporation
230 Constitution Drive, Menlo Park, CA
Tel: 650 473 7868
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 719 Std Error: 0.00.
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/db_xref="taxon:9606"
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         Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

- Goation of Lobrary was constructed by Life Technologies, a division of Invitrogen.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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17000600005410 GRN_PRENEU Homo sapiens CDNA 5', mRNA sequence...
CN272394
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                                                                                                                                                                                                                  Cot 25-normalized"
                                                                                                                                                                                                                                                                                                        40; Indels
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Pred. No. 4.3e-129;
0; Mismatches 40;
                                                                                                                                                         /organism="Homo sapiens"
|mol_type="mRNA"
|db_xref="taxon:9606"
|clone="CSODIO44YK06"
|tissue_type="placenta Cot
|plasmid="pcMVSPORT_6"
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Gaps

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194 306 254 366 314 426 374 486 434 546 494 909 554 999

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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Primer. It is trand cDNA was digested with Not I and cloned end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                         TSB bp mRNA linear EST 08-APR-2004
BX357208 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
Clone CS0D1022YJ18 3-PRIME, mRNA sequence.
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/mol_type="mRNA"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="CSODIO22V138"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 758)
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<u>ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTTTGCCTG</u>
                                 481 AGAGCACAGCGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODI022DE09NP1&c=4215.r. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On May 5, 2003 this sequence version replaced gi:30376125 Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.5%; Score 466.6; DB 5;
88.8%; Pred. No. 7.1e-124;
iive 9; Mismatches 43;
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1. (Dases 1 to 1071)

2. Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization

1. Unpublished (2001)

2. To May S. 2003 this sequence version replaced gi:30374869.

Contact: Genoscope Generican Generican Generican Genoscope - Centre National de Sequencage

2. Tue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE
Email: seqree Genoscope.cns.fr. Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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BX365066 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODI046YA18 3-PRIME, mRNA sequence.
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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/db_xref="taxon:9606"
/clone="CS0DI046YA18"
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                                                                                                                                                                                                   Homo sapiens (human)
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dI) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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full-length cDNA clone CS0DE013Y120 of Placenta of Homo sapiens
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTTCCTGTTGAGAGGGGGACTGAGAGAC
                                                                   301 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGGTGGAAGGTGACT
                                                                                                                                                                  GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
                                                                                                                                                                                              228 ACATCCACCITIAAACACGGGGCTIGCAACITAGCTCACACCAGCCAATCAGAGAGCTC
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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/organism="Homo sapiens"
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/mol type="mRNA"
/db xxef="taxon: 9606"
/clone="CSOBE013YI20"
/tissue type="Placenta"
/plasmid="pCMVSPORT_6"
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CR613169.1 GI:50493976
HTC; CNSLT_CDNA.
HOMO sapiens (human)
Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="mRNA"
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Genoscope - Centre National de Sequencage
2 rue Gastron Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Bmail: seqrefégenoscope.cns.fr, Web: www genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
4215.r
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/tissue type="PLACENYA COT 25-NORMALIZED"
/tissue type="PLACENYA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENYA COT 25-NORMALIZED"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299
                                                                                                                                                                                                                                                                                                                                                                                                                                                            520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACATCCACCTTTAAACACGGGGCTTGCAACTTRGCTCACACACAGACAATCAGAGAGAGT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACTAAAATGCTAATTAGGCAAAGACAGGAGGTAAAGAAATAGCCAATCATCTATTGCCT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Gatarrhini, Hominidae, Homo.
1 (Dases 1 to 1058)
14, W.B., Gruber, C., Jessee, J. and Polayes, D.
Pull-length cDNA libraries and normalization
Ompublished (2001)
On May 8, 2003 this sequence version replaced gi:30439129.
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52
                                                                                                                                                                                                                                                                                                                                                                                                           9
                                      /db_xref="taxon:9606"
/clone="CSODIOSIYN13"
/tissue_type="PLACENTA COT 25-NORWALIZED"
/clone="PLACENTA COT 25-NORWALIZED"
/clone="lst enrand cDNA was primed with a Not!-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was digested with Not! I and cloned into the Not! I and ECRN V
                                                                                                                                                                                                                       sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGAGCACAGCGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGAGCACAGCAGGAGGACAATGATCGGGATATAAACCCAAGTCTTCGAGCCGGCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCTAAGCCTAGGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGAAGCAGTTAGAGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGGACTGAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTTCCAGAATCAAAACTGTAAAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               cccrerarcritaaccrecrierraacrirgrercritecagaaregaagergraaaacra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCT
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                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                       15;
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                                                                                                                                                                                                                                                                                                      988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               m
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                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                       47;
                                                                                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                                                                                                 Score 454.2; DB :
Pred. No. 3e-120;
2; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BX378303.2 GI:46557492
                                                                                                                                                                                                                                                                                                      71.5%;
larity 89.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                            Local Similarity
wes 525; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300
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                                                                                                                                                                                                                                                                                                            Query Match
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KEYWORDS
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Matches
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AUTHORS
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.thml
Insert Length: 1645 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 475.
Location/Qualifiers
Irree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab.host="DH10B"
/clone lib="Soares testis NHT"
/clone lib="Soares T30-Pac" (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                     AA781423 494 bp mRNA linear EST 31-DEC-1998 aj26c03.81 Soares testis NHT Homo sapiens CDNA clone 1391428 3' similar to contains PTR7.tl PTR7 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGCTAGCCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAGGAAATCTCAA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 AAGAGGCTCACTAAAATGCTAATTAGGCAAAAACAGGAGGTAAAGAAATAGCCAATAAT 187
                                                                                                                   186 TIATTGCCTGAGAGTACAGCGGAAGGACAATGATCGGGATATAAACTCATGCATTCGAG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 494)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                          471 CTATTGCCTGAGAGCACAGGGGACAAGGATCGGGATATAAACCCAGGCATTCGAG
            -AGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCAT
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Pred. No. 2.5e-115;
0; Mismatches 36; Indels
                                                                                                                                                                           531 CCGGCAACGCCCCTTTGGGTCCCCTCTTGTATGGG 573
                                                                                                                                                                                                                    84
                                                                                                                                                                                                 126 CCACCAATGGCTACCCTTTTGGGTCCCCTCCTTTGTTATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="1391428"
                                                                                                                                                                                                                                                                                                                                                                                                             AA781423
AA781423.1 GI:2840754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.8%;
ilarity 92.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           al Similarity
458; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              sednence.
                 412
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Best Local
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Matches
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                    RESULT 14
AA781423/c
                                                                                                                                                                                                                                                                                                                                              DEFINITION
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AUTHORS
TITLE
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (102-AUG-2001) Asso Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi. Fu, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
Was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               606 TAATAGTTTCTTCAAATGGAGCACCTTATGCAGTCCATGACTAAGATCTACCATGGACCC 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGGACTATCTGGATTTCCTAGGCCAACTAAGAATCCCTAAGCCTAGGTGGGAAGGTGAC 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGACCGGCCTGCTAGCCCCATGCTCCGATGTTAATGACGTTGAAGGCACCCCTCCCGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAATCTCAACTGCAC-AACCCCTACTATGCCCCAATTCAGCGGAAGCAGTTAGAGCGG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCATCAGCCAACCTCCCCAACAGCACTTGGGTTTTTCCTGTTGAGAGGGGGGACTGAGAGA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGAAGGTGAC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 TGCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATC----- 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 666 ccnrigarictriaacgrectrigitaageritgietretecagaaregaagerigtaaaaca 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
troglodytes DNA, clone: PTB-130M15.F, genomic survey sequence
                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  486 gadatetedaetecedadaecetraetreerecedericageaggadeagerageegg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAACTGTAAAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Gaps
                                                                                                                                                                                Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 450.8; DB 9;
Pred. No. 2.7e-119;
0; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .689
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db xref="texon:5598"
/clone="PTB-130M15.F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                      AG121669.1 GI:16650834
GSS.
Pan troglodytes (chimpanzee)
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : pKS145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing: -21M13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tracking errors.
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88.3%;
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R.Site 1 : SacI
R.Site 2 : SacI
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double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
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Hegde, P., Oi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, T. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and Quackenbush, J.
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Contact: John Quackenbush
The Institute for Genomic Research
The Medical Center Dr., Rockville, MD 20850, USA 1=1: 301 838 3528
Fax: 301 838 0208
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                                                                                                                                   Query Match
Best Local Similarity 83.4%; Pred. No. 1.1e-114;
Matches 494; Conservative 19; Mismatches 66;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1019)
E 1, W.B., Gruber, C., Jessee, J. and Polayes, D.
FWI1-length cDNA libraries and normalization
Unpublished (2001)
On May 15, 2003 this sequence version replaced gi:30771765.

Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Z rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr. Web: www.genoscope.nns.fr
Ist strand cDNA was primed with a NotI-oligo(dT) primer
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
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|/organism="Homo sapiens"
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|/db_xref="taxon:9606"
|/db_xref="taxon:9606"
|/clone="CS0DE012YJ24"
|/tissue type="PLACENTA"
|/lone="CS0DE012YJ24"
|/lone="Tob="Homo sapiens PLACENTA"
|/nore="Vector: pCWYSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) prImer. Five prime end enriched,
                                             CTGCACAACCCCTACTATGCCCCCAATTCAGCGGGAAGCAGTTAGAGCGGTCATCAGCCAA
                                                                           GGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACTGCATCCACCT
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This sequence cluster 4215.r
Hots endemore belongs to sequence cluster, see
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODE012DE12NF1&c=4215.r.
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/cell_type="mononuclear lymphocyte"
/dev_stage="adult"
/dev_stage="adult"
/lab_host="E. coll SOLM'
/clone lib="Katze MMSP"
/note="Organ: spleen; Vector: Uni-ZAP XR; Site 1: EcoR I;
Site 2: Xho I; Created from Stratagene ZAP-CDNĀ Synthesis
kit [catalog #200400) and ZAP-CDNĀ Glapack III Gold
Cloning Kit (Catalog #200450)"
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Pred. No. 2.6e-113;
0; Mismatches 88; Indels 14;
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.02.24. 676 Q20 bases.
POR RAIMER CCCTCACTAAAGGAACAAAA
BACKWARD: CACTCATAGGGGAACTAAAA
INSERT LENGIH: 870 Std Error: 0.00
Plate: CLO00135 row: H column: 02
Seq primer: CCCTCACTAAAGGGAACAAAA
        USA
                                                                                                                                                                                                                                                                                                                                                                               /organism="Macaca mulatta"
|mol_type="mRNA"
|strain="Indian"
|db_rref="taxon:9544"
|clone="IBIUW:10227"
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ilarity 83.8%;
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(ercopithecinae, Macaca.

1 (bases 1 to 970)

Ratze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.

Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)

Contact: C. Magness
Illumigen Biosciences Inc.
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                                                                                          Location/Qualifiers
1.522
/ Caganism="Homo sapiens"
/mol_type="mRNA" serion 1.560"
/db_xref="taxon:960"
/clone lib="MAGE resequences, MAGE"
/note="Vector: pBluescriptSKm"
                                                                                                                                                                                                                                                                                                                                                                                          41;
                                                                                                                                                                                                                                                                                                                                      DB 2.;
                                                                                                                                                                                                                                                                                                                                      Score 432.4; DB 2;
Pred. No. 5.5e-114;
0; Mismatches 41;
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                                                                                                                                                                                                                                                                                                                                   68.1%;
91.8%;
                   Email: johnq@tigr.org
Plate: 292
Seq primer: Forward.
                                                                                                                                                                                                                                                                                                                                      Query Match 68.1
Best Local Similarity 91.8
Matches 479; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macaca mulatta
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Unpublished

(bases I to 653)

Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Pujiyama, Y., Watanabe, H. and Sakaki, Y.

Direct Submission
Submitted (102-MUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIERN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(B-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:sis 1-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                               1209 idcaccraccrataaacacagacratitaraacicagcracacarcragacaarcagaag 1268
                                                                                                                                                                                                                                                                    1269 TARAGAGAGCTCATTAAAATACCAATTAGTCTAAAACAGGAGGTAAAGAAATA---AAT 1325
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Pan troglodytes DNA, clone: PTB-008021.F, genomic survey sequence.
AG033781
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buran troglodytes
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
241 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC
                                                                           301 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCT-GGGAAGGTGAC
                                                                                                                                                                                                                                  ---AGAGAGCTCACTAAAATGCTAATTAGGC-AAAAATAGGAGGTAAAGAAATAGCCAAT
                                                                                                                                                      360 IGCAICCACTCTAAACAIGGGGC--ITGCAACTTAGCTCACACGACCAATC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell type="lymphoblast"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-008021.F"
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R.Site 2 : SacI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapber-remail.nih.gov
Tissue Procurement: CLOWIECH
CDNA Library Preparation: CLOWIECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Meb Site:
Contact: (Dickson, Mark) med@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAL Plates 37 Row: m Column: 12 This clone has the following problem: retained intron. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1028
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                                                                                                                                                                04-MAR-2003
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Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (02-APR-2002) National Institutes of Health, Mammalian
Submitted (02-APR-2002) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA
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Pred. No. 1.9e-111;
0; Mismatches 75; Indels 18
                                                                                                                                                                     linear
                                                                                                                                                          1500 bp mRNA
Homo sapiens, clone IMAGE:4770655, mRNA.
BC026287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol type="mRNA"
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/clone="INAGE:4770655"
/tissue type="Placenta"
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/note="Vector: pDNR-LIB"
                                                                   766 GCTCAAAAAAACATATTAAAAAATAAAA 794
                                    607 TCTTGCAACTGAAAAAAAAAAAAAAA
                                                                                                                                                                                                                              3C026287.1 GI:22382161
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ilarity 85.7%;
Conservative
                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Cl
Mammalia, Eutheria, P.
1 (bases 1 to 1500)
Strausberg,R.
                                                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 557; Conserv
                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                       DEFINITION
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TITLE
JOURNAL
                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                  REFERENCE
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COMMENT
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BE712673 11H_MGC_21 Homo sapiens CDNA clone IMAGE:3925728 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71
Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1407 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 455
POLYA-No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGGAAGCAGTTAGAGCGGTCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACTGCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGGCCTGCTAGCCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAGGAAAT
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0
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                   65.5%; Score 415.8; DB 1; larity 92.9%; Pred. No. 3.5e-109; Conservative 0; Mismatches 33;
                                                                                                                     1. .490
/organism≃"Homo sapiens"
                                                                                                                                               /mol_type="mRNA"
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/clone="IMAGE:2167578"
                                                                                                       Location/Qualifiers
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BE732673
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Best Local Similarity
Matches 435; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. D. D. D. Sequencing by: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                          580
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I (Dasea I to 490)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)

Contact: Robert Straueberg, Ph.D.
                                                                               9
                                                                                                   CCTGTTTCTTTAACCCCCGTTGTTAAGTGTGTCTCTNCCAGAATCANAGCTGTAAAGCTA
                                                                                                                                                                                                                          creencesectricariscrearistrantareacareandse-secencereas
                                                                                                                                                                                                                                                                                       475 AAAATCTCAACTGCACAACCCCTACTACACCCCCAGTTCAGCAGGAAGCAGTTAGAGTGGT
                                                                                                                                                                                                                                                                                                                                                                            AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                      GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCA-GAGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     295 ACATCCACCTTTAAACATGGGGCTTGCAACTTAGCTCACCCAACCAGTAAGGAGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATTGCCT
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                                                                                                                                                                 CTGGACCGGCCTGCTAGCCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
                                                                                                                                                                                                                                                          GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
                                                  Gaps
                                                   18;
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                      Length 653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 423; DB 9;
Pred. No. 3e-111;
0; Mismatches 52
                                                                                CCTGTATCTTTAACCTCC-TTGTTAAGTTTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIS98135.1 GI:4607183
EST.
                      66.6%;
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Homo sapiens
                        Query Match 66.6
Best Local Similarity 88.0
Matches 511; Conservative
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LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
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COMMENT
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/tisque_type="Islets of Langerhans"
/tisque_type="Islets of Langerhans"
/dev stage="Adult"
/lab host="DH108"
/clone lib="Melton Normalized Human Islet 4 N4-HIS 1"
/clone lib="Melton Normalized Human Islet 4 N4-HIS 1"
/clone lib="Melton Normalized Human Islet 4 N4-HIS 1"
/note="Organ: Pancreas; Vector: pSPORT; Site_1: Not 1;
Site_2: Sal 1: Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). CDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on Solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
library."
                        BIS63185 543 bp mRNA linear EST 12-MAR-2002 ie57c10.x1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens cDNA clone IMAGE:5670930 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 CTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAGGAAATCTCAACTG 193
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: dmalton@diohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Library was constructed by Dr. Douglas Melton for information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov
High quality sequence stop: 451.
                                                                                                                                                                                                                                    Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 543)
                                                                                                                                                                                                                                                                                                          1 (Dases 1 to 543)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R.,
Williams, T., Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5670930"
                                                                                                                                     BI963185.1 GI:16337590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Both"
                                                                                                                                                                                              Homo sapiens (human)
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Best Local Similarity 88.3'
Matches 467; Conservative
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Fax: 617-495-8557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_txefe="txxxon:9606"
/clone="txfefe="txxon:9606"
/clone="type="choriocarcinoma"
/lab host="MIH MGC 21"
/clone lib="WIH MGC 21"
/clone lib="WIH MGC 21"
/clone lib="Thing conta; Vector: pOTB7; Site_1: Xho1;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/Xho1 sites using the following 5' adaptor: GGCACGAG(G). Size-selected >S00bp for average innert size 1.8kb. Library constructed by Ling Hong in the laboratory of Garald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

B. (Dases) 1 to 440)

S. NIH-MGC http://mgc.nci.nih.gov/.

Intional Institutes of Health, Mammalian Gene Collection (MGC)

L. (Ontada Institutes of Health, Mammalian Gene Collection (MGC)

L. (Ontada Institutes of Health, Mammalian Gene Collection (MGC)

L. (Ontada Institutes of Health, Mammalian Gene Collection (MGC)

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Inorte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: image.llnl.gov

Plate: LLCM752 row: j column: 01

High quality sequence stop: 440.

Location/Qualifiers
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94.1%; Pred. No. 7.4e-104;
ive 0; Mismatches 26;
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Toyiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Toyoki, Y., Matanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Submitted (02-AUG-2001) Asso Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
T-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mall:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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Pan troglodytes DNA, clone: PTB-046A08.R, genomic survey sequence.
AG058970
                                                                                                                                                          574 CCCIGIAICTITIAACCICCTIGITIAACITIGICTICCAGAATCGAAGCIGIAAAACIA 515
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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      Length 966;
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62.2%; Score 395.2; DB 5; 79.6%; Pred. No. 3.8e-103; ive 22; Mismatches 84;
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2 rue Gaston Cremieux, CP 5706 - 91057 EWRY cedex - FRANCE
Email: seqrefégenoscope.cns.fr. Web: www.genoscope.cns.fr
18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies,
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BX380176 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA COT 25-NORMALIZED Homo sapiens CDNA COT 35-BX380176.2

BX380176.2

GI:46834414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
                                                                      TITCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGAAGGTGACTGCATCCACCTCTA
                                                                                                                                                                                                                                                                                                                          374 AACATGGGGCTTGCAACTTAGCTCACACCCGACCAAT-----CAGAGAGCTCACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 AAATGCTAATTAGGCAAAAACAGGAGGTAAAGAAATAGCCAGTCATCTATCGCCTGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACAGCGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 cacaaggggggggggagargargargararaagrccagggrricaaggggagggarg
                                        CACAACCCCTACTATGCCCCCAATTCAGCGGGAAGCAGTTAGAGCGGTCATCAGCCAACCT
                                                                                                                                                          CCCCAACAGCACTTGGGTTTTTCCTGTTGAGAGGGGGGGACTGAGAGACAGGACTAGCTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (basel to 966)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Vall-length cDNA libraries and normalization
Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30460243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On May 8, 2003 this
Contact: Genoscope
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submitssion
Submitted (O2-AUG-2001) Asao Fujiyama, The Institute of Physical
Submitted (RENEW), Genomic Sciences Center (GSC);
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
(E-mail:chimpbes@ger.riken.go.jp, WE:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:B1-45-503-9170)
Tel:91-45-503-9111, Fax:B1-45-503-9170)
Tolones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGGCAACCCCT 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCATGCTCCGATGTTAATGACTTGAAGGCACCCT-CCCGAGGAAATCTCAACTGCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    651 GACCCCGAGATCCAGTCCATGACTAAAGACTACTGTGAACCCCTGGACTGGCCTGCTAGC
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       Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.9%; Score 393.2; DB 9;
88.1%; Pred. No. 1.4e-102;
ive 0; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-137E19.F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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R.Site 1 : SacI
R.Site 2 : SacI.
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                                                                                                                                                                                                                                                                                                                                                             clone tracking errors.
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                                                                                      Unpublished
2 (bases 1 to 701)
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Pan troglodytes
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                               Length 651;
                                                                                                                                                           1. .651
| organism="Pan troglodytes"
| mil type="genomic DNA"
| db xref="taxon:9598"
| clone="PrB-046A08.R"
| sex="male"
| cell type="lymphoblast"
| cell type="lymphoblast"
| cell type="lymphoblast"
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                                                                                                                                                                                                                                                                                                                                                                                          Query Match
62.2%; Score 394.8; DB 9;
Best Local Similarity 87.6%; Pred. No. 4.6e-103;
Matches 503; Conservative 0; Mismatches 57;
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                                                                          : pKS145
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: Saci
                               Sequencing: M13Rev
                                                                            Vector
R.Site 1
R.Site 2
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CSAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1375 Std Brror: 0.00
Seq primer: -40m13 fwd. ET from Amersham.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA837267 443 bp mRNA linear EST 31-MAR-1998 od26b10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1369051 similar to contains PTR7.tl PTR7 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                       307 ACCTGGGAAGGTGACCACTTCCACCTTTAAACACGGGGCTTGCAACTTAGCTCACACATG 248
                                                                                                Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 443)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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AA837267/c
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SP 1 (bases 1 to 609)

Totoki, Y., Watanabe, H. and Sakaki, Y.

Totoki, Y., Watanabe, H. and Sakaki, Y.

Totoki, Y., Watanabe, H. and Sakaki, Y.

Totoki, Y., Watanabe, H. and Sakaki, Y.

Totoki, Y., Watanabe, H. and Sakaki, Y.

Submitted (02-AUG-2011) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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                                                                                                                          AGO66901 609 bp DNA linear GSS 03-NOV-200
Pan troglodytes DNA, clone: PTB-056L15.F, genomic survey sequence.
AGO66901
                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fuliyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
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/organism="Pan troglodytes"

/mol type="genomic DNA"

/db xref="taxon:9598"

/clone="PTB-056L15.F"

/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
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LIBRARY
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A1128526 Gares placenta 8to9weeks 2NDHP8to9W Homo sapiens cDNA clone IMAGE:1714147 3' similar to contains PTR7.bl PTR5 repetitive element;, mRNA sequence.
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                                                                                            /sex="male"
/clone lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGAGCCGGCAACGCCATTTGGGTCCCCTTCCTTTGTATGGGCGCTCTGTTTCA
                                                                                                                                                                                                                                                                                                                    CCGAGGAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGAAGCAGTTAGA
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                                                                                                                                                                                  DB 8;
                                                                                                                                                                                Score 387.2; DB 8;
Pred. No. 7.5e-101;
0; Mismatches 94;
                                               /mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3131 Col=8 Row=J"
                                 organism="Homo sapiens"
Location/Qualifiers
1. .712
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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: Jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3131 row: J column: 8
Seq primer: M13 Reverse
Class: BAC ends
High quality sequence stop: 712.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 712)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
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HS_3131_B2_E04_MR_CIT_Approved Human Genomic Sperm Library D Homo
saplens genomic clone Plate=3131 Col=8 Row=J, genomic survey
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                                                                                                                                             CAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGACAGG
                                                                                                                                                               ACTAGCTGGATTTCCTAGGCCGATTAAGAATCCCTAAACCTAGCTGGGAAGGTGACCGCA
                                                                                                                                                                                                                                                                                   184 ATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGGAAGCAGTTAGAGCGGTCAT
                                                                                                                                                                                                        ACTAGCTGGATTTCCTAGGCCAACGAAGCATCCCTAAGCCTAGCTGGGAAGGTGACTGCA
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                                                    Gaps
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                    1,
                      Length 443;
                                                    Indels
                    Score 392.6; DB 1;
Pred. No. 1.8e-102;
0; Mismatches 25;
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                      61.8%;
94.1%;
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Homo sapiens
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Matches 418; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 446).
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
AI393478.1 GI:4223025
                            Homo sapiens (human)
                                                                                                                        Tumor Gene Index
Unpublished (1997)
                                          Homo sapiens
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: ragabber-semail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 720 Std Error: 0.00.
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 428.
Location/Qualifiers
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                                                                                                                                          1. .436
/organiam="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1714147"
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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/clone_1bb="Soares_NPL_T_GBC_S1"
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a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI CGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-320897, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs r@mail.nih.gov

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1061 Std Error: 0.00

Seq primer: -40UP from Gibco
High quality sequence stop: 445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 AATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGAAGCAGTTAGAGCGGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 TCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            423 TAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATTGCCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCACAGGGGAGGGACAAGGATCGGGGATATAAACCCAGGCATTCGAGCCGGCAACGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 AGCACAGCAGGAGGACAAGGATCGGGATATAAACCCGGGCATTCAAGCCGGCAATGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       543 ACCCCCTTTGGGTCCCCTCCCTTTGTATGGCCGCTCTGTTTTCACTCTATTTCACTCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    326 GACTAGCTGGATTTCCTAGGCCGACTAAGAATCCCTAAGCGTAGCTGGGAAGGTGACTGC
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                                                                                                                                                                                                                   1. .446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
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EST 30-MAR-1999

446 bp mRNA linear ES:
tg45g04.x1 Soares NFL T GBC_S1 Homo sapiens cDNA clone
IMAGE:2111766 3', mRNÄ sequence.

A1393478

ACCESSION

DEFINITION

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a modified polylinker; Site_1: Not 1; Site_2: Eco RI;
a modified polylinker; Site_1: Not 1; Site_2: Eco RI;
a modified polylinker; Site_1: Not 1; Site_2: Eco RI;
Ilbraries (fetal lung NbH1J9W, testis NHT, and B-cell
lbraries (fetal lung NbH1J9W, testis NHT, and B-cell
NCL_GGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified CDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731339. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Addition 485 bp mRNA linear EST 03-MAR-2000 hd45h03.x1 Soares NFL T GBC_S1 Homo sapiens cDNA clone IMAGE:2912501 3' Bimilar to contains L1.t2 L1 repetitive element ;, AW511366
                                                                                                                                     221
                                                                                                                                                                                495
                                                                                                                                                                                                                             162
                                          281
                                                                                        437
                                                                                                                                                                                                                                                                           555
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 485)
NCI-GARP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLML ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco High quality sequence stop: 470.

Location/Qualifiers
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                                                                                        386 GCAACTTAGCTCACACCCGACCAATC----AGAGAGCTCACTAAAATGCTAATTAG
                                                                                                                  CGAAGAATCCCTAAGCCTGGG-AAGGTGACTGCATCCACCTCTAAACATGGGGCTT
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                77
                                                                                                                                                                                                                                                                                                                                                                                                  CCCCTCCCATTGTATAGGAGCTCCG
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Best Local S
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AW511366/c
LOCUS
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Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
BAC end sequences of Library PTB
Upublished

E (bases 1 to 641)

E 2 (bases 1 to 641)

S Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suchiro-chou, Tsurumi-ku, Yochama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-911, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
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                                                                                                                                               GSS 01-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              520 AATGTTGATGACATTGAAGGCACCCCTCCCAAGGAAATCTCAACTGCGCGACCCCTACTA 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCCCCAATTCAGCGGAAGCAGTT-AGAGCGGTCATCAGCCAACCTCCCCAACAGCACT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341
                                                                                               641 bp DNA linear GSS 01-NOV-200 An troglodytes DNA, clone: PTB-012009.F, genomic survey sequence. AG036829 AG036829.1 GI:16563702 GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTGTCTCTTCCAGAATCGAAGCTGTAAAACTACAAATCGTTCTTCAAATGGAGCCCCAG 581
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                                                                                                                                                                                                                                                                                                          Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .641
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       Location/Qualifiers
                                                                                                                                                                                                                                                            Pan troglodytes (chimpanzee)
Pan troglodytes
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R.Site 1 : SacI
R.Site 2 : SacI.
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                                                                                                                                                                                            ACCESSION
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KEYWORDS
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                                                                                                      RESULT 31
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556 bp mRNA linear EST 05-AUG-2002 PLACE3 Homo sapiens cDNA clone PLACE3000382 3', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGAGAGGGGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 556) (bases 1 to 556
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                                                                                                                  40 AGAATCAAAACTGTAAAACTACAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATG
                                                                                                                                                                 564 AGAATCAAAGCTGTAANACAACATCGTTCTTCAAATGGAGCCCCAGATGCAGTCCATG
                                                                                                                                                                                                                ACTAAGATCCACCGTGGACCCCTGGACCGGCCTGCTAGCCCCATGCTCCGATGTTAATGAC
                                                                                                                                                                                                                                                                    604 ACTAAGATCTACCGCGGATCCCTGGACCAGCCTGCTAGCCCCATGCTCGATGTTAATGAC
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Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Score 379.8; DB 5;
Pred. No. 1e-98;
             59.8%; Score 379.8; ilarity 84.3%; Pred. No. 1e-9 Conservative 0; Mismatches
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Unpublished (2000)
Contact: Takao Isogai
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DKFZp686M05227-5', mRNA sequence.
                                                                                                                                                                                                                                                                         377
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Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (baees I to 664)
Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wismann, S.
EST (Bahr, A., Lauber, J., Mewes, H.W., Weil, B., et al.)
                                                                                                                                                                         317
                                                                                                                                                                                                                  AGCAGCACTTGGGTTTTCCTGTTGAGAGCGGGGACTGAGAGACAGGACTAGCTGGATTTC 301
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                    CACATGCTCCGATGTTAATGACATCGAAGGCACCCGTCTCGAGGAAATCTCAACTGCACA 421
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Wolecular Genome Analysis, German Cancer
Clone from S. Wiemann, Wolecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidalberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKFZp686W05227) is available at the RZPD in Berlin.
Please contact the RZPP: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GRRWANY; Email: clone@rzpd.de.
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/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
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                                                                        ACCCCTACTATGCCCCCAATTCAGCGGAAGCAGTTAGAGCGGTCATCAGCCAACCTCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
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/lab_host="DH10B"
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AUTHORS
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ACCESSION VERSION KEYWORDS SOURCE

FEATURES

ORIGIN

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Contact: Robert Strausberg, Ph.D.
Email: Ggapbs-r@mail.nih.gov
Tissue Procurement: Dr. Elice Spindel
Tissue Procurement: Dr. Elice Spindel
CDNA Library Preparation: CLONTECH
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CEAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM3133 row: i column: 17
High quality sequence stop: 373.
High quality sequence stop: 373.
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                                                               (CGAP),
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Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.

1 (bases 1 to 865)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP cancer Institute, Cancer Genome Anatomy Project (Chunor Gene Index (1997))
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Matches 458; Conservative 0; Mismatches 49; Indels 19
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IMAGE:6884154 5', mRNA SEQUENCE.
CB231128
CB231128.1 GI:28282706
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 AATCAGGTAGCAAAGAGAGCTCGTTAAAATGATAATTAGGCAAAAACAGGAGGTAAAAA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    518
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                                                                                                                                                                                                                                                                                                                                          AACTGTAAAACTACAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGAT 107
                                                                                                                                                                                                                                                                                                                                                                      540 AACTNGTAAACTTNCAATCGTTCTTCAAA-GGAGTCCCCGATNCAGTCCATGATTAAGAC 482
                                                                                                                                                                                                                                                                                                                                                                                                       CCACCGTGGACCCCTGGACCGGCCTGCTAGCCCCATGCTCGATGTTAATGACATTGAAGG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGAAG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macaca mulatta (rhesus monkey)
Macaca mulatta
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31
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                  Fax: 81-438-52-3986
Email: genomics@hi.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGTTAGAGCGGTCATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGG
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                                                                                                                                                                                                                                                                                                              39;
                                                                                                                                                                                                                                                                                 Length 556;
                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                              50;
                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                              Query Match

59.1%; Score 375.2; DB

Best Local Similarity 84.1%; Pred. No. 2.1e-97

Matches 470; Conservative 0; Mismatches 55
                                                                                                                         1. .556
/organism="Homo sapiens"
/organism="mRNA"
/db xref="taxon:9606"
/clone="PLACE300382"
/clone lib="PLACE3"
/clone lib="PLACE3"
/note="Vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTTTTCACTCTATTTCAC 597
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ORGANISM
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Direct Submission
Claydo-2001) Asao Fujiyama, The Institute of Physical
and Chamical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gac.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               416
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                                                                                                                                                                                                                                                                                                                                                                                                       GSS 03-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                 AGU76758 679 bp DNA linear GSS 03-NOV-200
Pan troglodytes DNA, clone: PTB-071A23.R, genomic survey sequence.
AG076758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                     52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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                                                                                                  1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fujjyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 364.8; DB 9; Length
Pred. No. 2.3e-94;
0; Mismatches 42; Indels
                                                                                                                                                                                                                   593
                                                                                                                                                                                                                                                                   51 cccrcrcrrrcrardegaccrcrcrrrrcacrcrarr 15
                                                                                                                                                                                                                CCCTCCCTTTGTATGGCGCTCTGTTTTCACTCTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic_DNA"
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/clone="PTB-071A23.R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .679
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Pan troglodytes
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: Saci
: Saci.
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larity 90.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vector :
R.Site 1 :
R.Site 2 :
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Best Local Si
Matches 390
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                                                                                                                                                                                                                                                                                                                                                       RESULT 37
AG076758/c
                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
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JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
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1. .470

/organism="Homo sapiens"
/mol_type="mRNA"
/do_type="mRNA"
/do_type="mRNA"
/do_type="Ronison:9606"
/clone="InMAGE:1662921"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
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/note="Organ: mixed (see below); Vector: pT7T3D-Pac
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
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/note="Organ: mixed (see below); Vector: pT7T3D-Pac
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/note="Organ: mixed (see below); Vector: pT7T3D-Pac
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/note="Organ: mixed (see below); Vector: pT7T3D-Pac
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/note="DT7T3D-Pac
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                                                                                                           A1074704 Soares NHHMPu S1 Homo sapiens cDNA clone IMAGE:1662921 3' similar to contains PTR7.t2 PTR7 repetitive element ;, mRNA
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1 (bases 1 to 470)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATional Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 Fwd. ET from Amersham
High quality sequence stop: 447.
Location/Qualifiers
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                                                                                                                                                                                                                                                        AI074704.1 GI:3401348
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                                                              RESULT 36
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qc61e08.x1 Soares placenta 8to9weeks_2NbHP8to9W Homo sapiens cDNA
clone IMAGE:1714118 3' similar to contains PTR7.t1 PTR7 repetitive
                                                                                                          301 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT 360
                                                                                                                                   175 AGGACTAGCTGGATTTCCTAGACCGACTAGGATCCCTAAGCCTAGCTGGGAAGGTGACC 116
                                                                                                                                                                361 GCATCCACCICTAAACAIGGGGCIIGCAACIIAGCICACACCGACCAAICAGAGGCIC 420
                        236
                                                      300
                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primateß; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 415)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                             26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1184 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 413.
Location/Qualifiers
                                                                                                                                                                                GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
                295 GAAATCTCAACTGCACAACCCCTACCATGCCCCATTTCAGCAGGAAGCAGGTAGAGGGT
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                                                       CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGA
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AI128496
AI128496:1 GI:3597010
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Homo sapiens
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Matches 389; (
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Upbases 1 to 777)

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Tol. 22 Suchiro-chou, Tsurumi-ku, Vokohama, Kanagawa 230-0045, Japan
(E-mall:chimpbeseger.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AG030228 777 bp DNA linear GSS 01-NOV-2001
Pan troglodytes DNA, clone: PTB-002I20.R, genomic survey sequence..
AG030228
                                                                                                                                                                                                          442
                                                                                                                                                                                                                                443 AATAGGAGGTAAAGAAATAGCGAATCATCTATTGCCTGAGAGCACAGCGGGGGGACAAG 502
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297
                                                                                                                                CCAACGAAGAATCCCTAAGCTGGGAAGGTGACTGCATCCACCTCTAAACATGGGG 382
                                                                                                                                                                       237
                                                         GAGAGGGGGACTGAGAGACAGGACTAGCTGGATTTCCTAGG 322
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTTGTATGGGGGCTCTGTTTTCACTCTATTACACTCTATTAAATCTTGCAACTG 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Pan troglodytes"
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/db_xref="taxon:9598"
/clone="PTB-002I20.R"
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Pan troglodytes
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                                                                  CACTTGGGTTTTCCTGTT
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R.Site 2
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AG030228/c
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/mol_type="mRNA" /db_xref="taxon:9606" /clone="INAGE:2164384" /Lissue_type="anaplastic oligodendroglioma" /lab.host="DH10B"

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Insert Length: 1440 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stopp: 414.
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Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                    cccrararcriraaccrcrirgriragririgicricricgaarcaaagcrecaaaacre 456
                                                                                                                                                            120
                                                                                                                                                                                 CAAATCATTCTTCAAATGGAGCCCCAGATGCAGTCTATGACTAAGATCTTCCGTAGACC 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC 420
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 425)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAtional Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index
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                                                                                                                                                            CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
                                                                                                                                                                                                                                         CTGGACCGGCCTGCTAGCCCCATGCTCCGATGATGACATTGAAGGCACCCCTCCCGAG
                                                                                                                                                                                                                                                                  CTGGACCAGCCTGCTAGCCCATGCCCCAATGTCAATGACATCGAAGGCACCCCTCCCGAG
                                                                                                                                                                                                                                                                                                                         181 GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
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                                       Gaps
                                       ö
  Length 777;
                                       Indels
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  DB 9;
Score 360.6; DB 9
Pred. No. 3.9e-93,
0; Mismatches 64
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A1570707
A1570707.1 GI:4534081
  56.8%;
86.2%;
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Query Match 56.8
Best Local Similarity 86.2
Matches 399; Conservative
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Search completed: February 21, 2005, 14:51:02 Job time : 1986.67 secs

/organism="Homo sapiens"

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Date 1 (Dases 1 to 1481)

Baccala,G.P., Pradel,F.K., Bedin,F., Sodoyer,M., Ott,C., Mallet,F.,
Perron,H. and Mandrand,B.

Retroviral nucleic material and nucleotide fragments, in
particular, associated with multiple sclerosis and/or rheumatoid
arthhitis, for diagnostic, prophylactic and therapeutic uses
Patent: JP 2002509437-A 7 26-MAR-2002;
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JP 2002509437-A/7
26-MAR-2002
20-JUL-1999 JP 1999508255
07-JUL-1997 FR 97/08816
GLAUCIA PARAHNOS BACCALA, FLORENCE KOMURIAN PRADEL, FREDERIC
                                             Ното варі
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                                                                                                                                                           Sequence
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Retroviral nucleic material and nucleotide fragments, in
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AF520520 F
AF520522 F
AF520530 F
AF520562 F
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CC associated with multiple sclerosis and/or rheumatoid arthritis,
CC diagnorities
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Location/Qualifiers
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Strandedness: Single;
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AF52048782
AF52048982
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AF520483S2
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JP 2002509437-A/7.
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BD136197
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AF127228 Multiple
AL390039 Human DNA
CQ71948 Sequence
BD252040 Method fo
AX036992 Sequence
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AC023366 Homo sapi
AX478550 Sequence
AX101580 Gorilla g
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AX101593 Hylobates
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11288.850 Million cell updates/sec
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                                                                                                             February 21, 2005, 06:32:54 ; Search time 6356.91 Seconds
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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length: 2000000000
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Unclassified.
Unclassified.
I (bases 1 to 1481)
Perron, H., Beseme, F., Bedin, F., Paranhos-Baccala, G.,
Komurian-Pradel, F., Jolivet-Reynaud, C. and Mandrand, B.
Komurian-Pradel, F., Jolivet-Reynaud, C. and Mandrand, B.
Isolated nucleotide sequences associated with multiple sclerosis rheumatoid arthritis and a process of detecting rathritis and a process of detecting patent: US 682703-A 105 24-JUN-2003;
Location/Qualifiers
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                                                                                                       CTCAGCCAATGGATGCCCTGGGTTCTCCTTAGGACCTCTAGCAGCTCTAATATTG
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                                 GGAGAAGAACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAA
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CTTCCTTTTGTTATCAGAGGAGGAGTGCTAGGCAGACTAGGTACTGGCATTGGCAGTATC
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Pred. No. 0;
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Sequence 105 from patent US 6582703.
AR344387.1 GI:33740328
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/mol_type="mRNA"
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Best Local Similarity 100.
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    /organism="unidentified"
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    /db_xref="taxon:32644"

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llarity 100.0%; Pr
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RESULT 4 AF127228 AF127228 1932 bp mRNA linear VRL 11-AUG-1999 LOCUS DEFINITION Multiple sclerosis associated retrovirus element clone CL15 env-like mRNA sequence. ACCESSION AF127228 VERSION AF127228.1 GI:5726293	Multiple sclerosis associated retrovirus element Nultiple sclerosis associated retrovirus element Viruses; Retroid viruses; Retroviridae. E (bases 1 to 1932) S Komurian-Pradel, F., Paranhos-Baccala, G., Bedin, F., Ounanian-Paraz, A., Sodoyer, M., Ott, C., Rajoharison, A., Mallet, F., Mandrand, B. and Perron, H.	TITLE Molecular cloning and characterization of maky-related Sequences associated with retrovirule-like particles JOURNAL Virology 260 (1), 1-9 (1999) MEDLINE 99335590 PUBMED 10405350 REFERENCE 2 (bases 1 to 1932) AUTHORS Komutian-Pradel, F., Paranhos-Baccala, G., Bedin, F., Authors Authoranian-Paraz A., Sodover, M., Ott.C., Raioharison, A., Garcia, E.,	Mallet, F., Mandrand, B. and Perron, H. TITLE Direct Submission JOURNAL Submitted (10-EEB-1999) UMR103 CNRS, bioMerieux, 46, allee D'Italie, Lyon 69007, France FEATURES Location/Qualifiers	<pre>source 11932 /organism="Multiple sclerosis associated retrovirus element"</pre>	peptide region, and partial peptide region, and partial a card cu37-14; results in a Trp amino acid translation'	00, I		OY 61 GCACCCTCCATGCTGCTGTACAACCAGTAGCTCCCCTTACCAAGAGTTTCTATGAAGA 120		QY 181 ACCTTCACTGCCACACCCATATGCCCGCAACTGCTATAACTCTGCCACTTTTGCATG 240	OY 241 CATGCAAATACTCATTATTGGACAGGGAAAATGATTAATCCTAGTTGTCCTGGAGGACTT 300	OY 301 GGAGCCACTGTTGGACTTACTTCACCCATACCAGTTGTCTGATGGGGTGGAATT 360
361 CAAGGTCAGGCAAGAAAAACAAGTAAAGGAAGCAATCTCCCAACTGACCGGGGGACAT 420 421 AGCACCCCTAGCCCTACAAAGGACTAGTTCTCTCAAAACTACATGAAACCCTCCGTACC 480 421 AGCACCCCTAGCCTAAAAGGACTAGTTCTCTCAAAAACTAACT		GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACCTCACCTGTGTA GGACCTCTTGTTTCCAATCTGGAAATAACCCCATACCTCAAACCTCACTGTGTA GGACCTCTTGTTTCCAATCTGGAAATAACCCCATACCTCAAACCTCACGTGTGTA AGCAATACTATAGACACAACCAGCTCCCAATGCATCAGGTGGGTAACACCTCCC	TGTTTG	841 AATGGCTCTTCAGAATCTATGTGCTTCCTCTTTTAGTGCCCCCTATGACCATCTAC 900 841 AATGGCTCTTCAGAATCTATGTGCTTCCTTCTTAGTGCCCCCTATGACCATCTAC 900 841 AATGGCTCTTCAGAATCTATGTGCTTCCTTCTTTTTAGTGCCCCTTTTAGACCATCTAGCCATTAGACCATTTATACAATCTAGTCGTAGCCCCCAACAAAAAGAGTACCATT 960 901 ACTGAACAAGATTTATACAATCATGTCGTACCTAAGCCCCCAACAAAAAGAGTACCCATT 960 901 ACTGAACAAAATTATAATACAATCATGTCGTACCCTAAGCCCCCAACAAAAGAGTACCCATT 960	961 CTTCCTTTTGTTATCAGAGCAGGAGTGCTAGGCAGACTAGGTACTGGCAGTATCGCAGTATC 1020	ACAACCTCTACTCAGTTCTACTACTATTCTCAAGAATAAATGGTGACATGGAACAG GTCACTCTACTCCTGGTCACTTGCAAGATTAACTCCCTAGGAGGAGTGGTCCTT GTCACTCACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGGAGGGGTGTTTTTTTT	1141 CAAAATGGAAGAGTTTAGACTTGCTAACGGCCAAAAGAGGGGGAACCTGTTTATTTTA 1200 	1201 GGAGAAGAACCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAA 1260 	1261 ATTCGAGATCGAATACAATGTAGAGGAGGTTCAAAACACCGAACGCTGGGGCCTC 1320 	1321 CTCAGCCAATGGATGCCCTGGGTTCTCCCCTTCTTAGGACCTCTAGCAGCTCTAATATTG 1380	1381 ITACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATT 1440 	1441 GAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAACCCCA 1481

Oy 1441 GAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAACCCCA 1481	AL390039/c LOCUS AL390039 LOCUS AL390039 DEFINITION Human DNA sequence from clone RP13-383KS on chromosome XQ22.1-24	Contains ESTs, STSs and GSSs. Contains a novel gene and a novel gene similar to NUP62 (nucleoporin 62kD), complete sequence. ACCESSION AL390039.10 GI:10186780	HTG; nucleoporin; Mr Homo sapiens (human) Homo sapiens Eukarvota: Metazoa;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 162579) ATTHORS Graffam, D. ATTHORS Dispert Submission	JOURNAL Submitted (19-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire, JOURNAL Submitted (19-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonarequestsGeanger.ac.uk		corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. The following abbreviations are used to associate primary accession mumbers given in the feature table with their source databases:	Em: , EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human	chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrx thompspany. This seminance is not the entire insert of clone	RP13-383KS It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP13-383KS is at 1 in this sequence. The true left and of clone RP13-383KS is at 15480 in this sequence.	This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known such as compressions and repeats, but not necessarily within known such as companies and repeats within known the sequence is	ambiguous, there is an amotation using the 'unsure' feature key. RP13-183KS is from the library RPCI-13.2 constructed by the group of Pater de Jong. Por further details see http://www.chori.org/hacmac/home.htm	VECTOR: pBACe3.6. FEATURES Location/Qualifiers 1. 186259	/ organization of the control of the	/mg/ /clone="RP13-383K5" /clone lib="RPCT-13.2" misc_feature	. GSS: Em:AQ504848"	9 g
** 161 CAAGGTCAGGCAAGAAAAACAAGTAAAGGAAGCAATCTCCCAACTGACC	AAAACTACATGAAACCCTCCGTACC	Qy 481 CATACTCGCCTGGTGAGCCTATTTAATACCACCCTCACTCGGCTCCATGAGGTCTCAGCC 540 D	OY 541 CAAAACCTACTAACTGTTGGATGTGCCTCCCCTGCACTTCAGGCCATACATTTCAATC 600	Oy 601 CCTGTTCCTGAACAATGGAACTTCAGCACAGAAATAAACACCACTTCCGTTTAGTA 660 	Oy 661 GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACCTCACCTGTGTAAAATT 720	Oy 721 AGCAATACTATAGACACAACCAGCTCCCAATGCATCAGGTGGGTAACACCTCCCACACGA 780	OY 781 ATAGICTGCCTACCTCAGGAATATTTTGTCTGTGGTACCTCAGCCTATCATTGTTG 840	Qy 841 AATGGCTCTTCAGAATCTATGTGCTTCCTCTCATTCTTAGTGCCCCCTATGACCATCTAC 900 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 901 ACTGAACAAGATTATACAATCATGTCGTACCTAAGCCCCACAACAAAAGAGTACCCATT 960	OY 961 CITCCTTITGTTATCAGAGCAGAGTGCTAGGCAGACTAGGTACTGGCAGTATC 1020	Qy 1021 ACAACCTCTACTACTACTACAAACTATCTCAAGAAATAAAT	Oy 1081 GTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTT 1140	Qy 1141 CAAAATCGAAGATTTAGACTTGCTAACCGCCAAAGAGGGGGAACCTGTTTATTTTA 1200	Qy 1201 GGAGAAGACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAA 1260 	OY 1261 ATTCGAGATACAATGTAGAGAGGAGGTTCAAAACACCGAACGCTGGGGCTC 1320 	Qy 1321 CTCAGCCAATGGATGCCCTGGGTTCTCCCCTTCTAGGACCTCTAGCAGCTCTAATATTG 1380 Db 1772 CTCAGCCAATGGATGCCCTGGGTTCTCCCCTTCTTAGGACCTCTAGCAGCTCTAATATTG 1831	QY 1381 TTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATT 1440 1832 TTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATT 1891

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/note="LiMEC repeat: matches 1044. .1140 of consensus" 15885. .16086
/note="match: STS: Em:G34444 Em:L14259" 15920. .16082
/note="match: GSS: Em:AQ769824" complement(15927. .16073)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              420. .8487
noce="LIMC/D repeat: matches 5582. .5648 of consensus"
0039. .10396
noce="THEIB repeat: matches 1. .364 of consensus"
0519. .10807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="49 copies 2 mer ga 75% conserved"
018. .6409
note="LIPALS repeat: matches 5769. .6157 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           // mote="MIR repeat: matches 103. .186 of consensus"
3110. .1322
// mote="FLAM C repeat: matches 2. .124 of consensus"
// note="FLAM C repeat: matches 2131. .2414 of consensus"
// note="LIMEc repeat: matches 2131. .2414 of consensus"
// s519. .13853
// matches 1. .346 of consensus"
// 1864. .14039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="MERZO repeat: matches 1. .218 of consensus" 4255. .14807 note="LiMEz repeat: matches 1686. .1951 of consensus" 4808. .1510 repeat: matches 1. .311 of consensus" note="AluJb repeat: matches 1. .311 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="LIMB5 repeat: matches 5823. .6167 of consensus" .824. .15920 note="LIMBc repeat" -----
                                                                                                                                                                                                                                                                                                                                                                                                                     .5779 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="Allogy repeat: matches 3. .297 of consensus"
1343. 11416
note="37 copies 2 mer tt 67% conserved"
note="LIMD3 repeat: matches 7162. .7739 of consensus"
2030. 12337
note="Allox repeat: matches 1. .309 of consensus"
2995. 13077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="LiMbC repeat: matches 1309. .1686 of consensus"
5496. .15822
note="LiMbS repeat: matches 5823. .6167 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="LIMEc repeat: matches 1951. .2131 of consensus"
                                                                                                                                                                                                                                                                                                                                                       1989. .5149
/note="LiMAB repeat: matches 6120. .6288 of consensus"
5152. .5602
/note="LiPA15 repeat: matches 5325. .5779 of consensus
                                                                                                         consensus,
                                                                                                                                                                              1092. .4231

'note="LlM4 repeat: matches 612. .756 of consensus"

1373. .4559

1376-"LlMc repeat: matches 971. .1152 of consensus"

1586. .4619

'note="17 copies 2 mer aa 100% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     566. .6750
note="LiM4 repeat: matches 2857. .3036 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             751. .7063 ... orde="Aludo repeat: matches 1. .307 of consensus" 064. .8097 ... orde="LIM4 repeat: matches 3036. .4105 of consensus"
1143. .1456
/nocte="AluSx repeat: matches 1. .312 of consensus"
1457. .2938
/nocte="LIMEc repeat: matches 356. .1897 of consensus"
                                                                                                                                                                                                                                                                                                                  623. .4964
note="MLT1A1 repeat: matches 3. .333 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                     %606. .5916
hnote="Alu8q repeat: matches 1. .313 of consensus"
5917. .6014
hnote="49 copies 2 mer ga 75% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      099. .8419
note="AluSx repeat: matches 1. .306 of consensus"
                                                                                                                                      844. .4087
note="Lim4 repeat: matches 1. .251 of consensus"
                                                                                       1922. 3739 note="LipA2 repeat: matches 5329, .6146 of note="LipA2 repeat:
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/note="LiMc/O repeat: matches 5620. .5805 of consensus"
77182. .2730
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Thote="HERV17 repeat: matches 4301. .4980 of consensus" 2228
12298 .22742
12298 .22743
123048
Thote="LiMB5 repeat: matches 5623. .6135 of consensus" 12743. .23048
Thote="Alux repeat: matches 1. .306 of consensus" 12049. .23286
123049. .23286
123285. .23361
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"note="MIR repeat: matches 1. .89 of consensus"
[1615. .26328
"note="MITIA1 repeat: matches 144. .352 of consensus"
[1654. .26697
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note="HERV17 repeat: matches 6812. .8523 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="LIM4 repeat: matches 5006. .5082 of consensus" 3364. .23429
note="LIM4 repeat: matches 4019. .4084 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="L1_repeat: matches 2600. .3097 of consensus"
25110. .25436
/note="L1M3 repeat: matches 5101. .5440 of consensus"
25437. .25742
/note="Matches" matches 1. .307 of consensus"
25779. .25961
                                                                                                                                                               17107. 17166

Anote="L2 repeat: matches 2688. .2750 of consensus"
17175. .17755

Anote="L2 repeat: matches 1244. .1898 of consensus"
7/note="L2 repeat: matches 148. .418 of consensus"
7/note="MER70A repeat: matches 148. .418 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="L1M4 repeat: matches 4019. .4084 of consensus"
3429. .24305
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                                                                                                                                                                                                                                                                                                                               18213. 18318

/note="L2 repeat: matches 1128. 1247 of consensus"

18706. 18811

/note="L2 repeat: matches 2631. 2750 of consensus"

8812. 19057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="AluSx repeat: matches 1. .297 of consensus"
19058. .19492
/note="L2 repeat: matches 2213. .2647 of consensus"
complement(19352. .19843)
/note="match: GSS: Em:AQ340313"
19556. .19872
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5962. .26059
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note="match: GSS: Em:AQ054794 Em:AQ823559"
                                                                                                         note="38 copies 2 mer at 71% conserved"
7107. .17166
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                                                                Em: AQ457003"
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Pred. No. 0;
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                                     16067. .16294
'note="match: GSS:
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Best Local Similarity 99.5%;
Matches 1473; Conservative
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us-09-319-156b-9.rge

Db 1476 GAAGCTGTAAAGCTACAAA	RESULT 7 BD252040 LOCUS DEFINITION Method for detecting	ACCESSION BD252040 VERSION BD252040.1 GI:330618 KEYWORDS JP 2002539804-A/l. SGIRCE HOMO BRDIENS (Inuman)		AUTHORS Perron, H. and Lafont, TITLE Method for detecting JOURNAL Patent: JP 2002539804 HIO MEREUX	COMMENT OS Homo sapiens (hu PN JP 2002539804-A/ PD 26-NOV-2002 PF 20-MAR-2000 JP 2	PR 19-MAR-1999 FR HERVE PERRON, MONIQUE PC CIZNIS/09, A61K31 PC A61P25/00,	PC C07K14/47,C07K16 G01N33/15, PC G01N33/569,	(C12Q1/O2,C12R1:93), A61K37/O2 CC Method for detect	FH Key FT Source FT Location/Out	source 11629 /organism="! /mol_type="" /db xref="t	ORIGIN Query Match Rest Local Similarity 99.2%;	Matches 1469; Conservative Oy 1 ATGCCCTCCTTATCAT	Db 1 ATGGCCCTCCTTATCATY Qy 61 GCACCCCCTCCATGCTGC	61	Oy 121 ACGCGCTTCCTGGAAAT.	181	Db 181 ACCTTCACTGCCCACACC Oy 241 CATGCAAATACTCATTAT	241 CAIGCAAATACTCATTAT 301 GGAGCCACTGTCTGTTGG	
361 CAAGGTCAGGCAAGAGAAAACAAGTAAAGGAAGCAATCTCCCAACTGACCCGGGGACAT 420 	AGCAC AGCAC	481 CATACTCGCCTGGTGAGCCTATTTAATACCACCCTCACTCGGCTCCATGAGGTCTCAGCC 540	541 CAAAACCCTACTAACTGTTGGATGTGCCTCCCCCTGCACTTCAGGCCATACATTTCAATC 600	601 CCTGTTCCTGAACAATGGAACTTCAGCACAGAAATAAACACCACTTCGTTTTAGTA 660 	661 GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACCTCACCTGTGTAAAATTT 720 	721 AGCAATACTATAGACACAACCAGCTCCCAATGCATCAGGTGGGTAACACCTCCCACACGA 780 	781 ATAGICIGCTACCTCAGGAATATITIGICIGGGACCTCAGCCTAICAITGITG 840	841 AATGGCTCTTCAGAATCTATGTGCTTCCTCTCATTCTTAGTGCCCCCTATGACCATCTAC 900	901 ACTGAACAAGATTATACAATCATGTGGTACCTAAGCCCCACAAAAGAGTACCCATT 960 	961 CTTCCTTTTGTTATCAGAGGAGTGCTAGGCAGACTAGGTACTGGCATTGGCAGTATC 1020 	1021 ACAACCTCTACTCCACTTCTACTACAAACTATCTCAAGAAATAAAT	1081 GTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTT 1140		GGAGAAGAAGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAA 126	1236 GGAGAAGAATGUTTATTATTATTATTAATCAATCCAGAATTGTCACAGAATGTTAAAGATAAGAA 1295 1236 JAHASAAGATGTTATTATTAGTTAATCAAATCAAATTGTAAATGAATG	ATTCGAGATCGAATACAATGTAGAGCAGAGGACTTCAAAACACCGAACACTGGGGCCTC	1321 CTCAGCCAATGGATGCCCTGGGTTCTCCCCTTTAGGACCTCTAGCAGCTCTAATATTG 1380	TTAC	
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                                                                                                    1629 bp DNA linear PAT 17-JUL-2003 superantigen activity in a biological sample.
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99/03622,28-OCT-1999 FR 99/13755 PI
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31/711,A61K38/00,A61K39/395,A61K45/00,A61K48/00,
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),(C12Q1/68,C12R1:93),C12N15/00,GQ1N27/26, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                       16/18,C12N7/00,C12Q1/02,C12Q1/68,G01N27/447, PC
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                                                                                                                                                                                                            Chordata, Craniata, Vertebrata, Euteleostomi;
Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                              .,M.
; superantigen activity in a biological sample
)4-A 1 26-NOV-2002;
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1. .1629
/organism='Homo sapiens (human)'.
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0; Mismatches
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"genomic DNA"
"taxon:9606"
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Marcy

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/db xref="GI:13310191"
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GNIDAPSYRELSKGNSTFTAHTHMPRNCYMSATLCHHSTPSTPSPYKGLVLSKLHETLRT
TVCMTYFTHTSWSDGGGTORATHVTWMCWATCHSTSPYTSPYTSVLHETLRT
TVGPLVSNLEITHTSNLTCVKFSNTIDTTSSQCIRWTTPPTRIVCLESGIFFVCGTSA
LVGPLVSNLEITHTSNLTCVKFSNTIDTTSSQCIRWTTPPTRIVCLESGIFFVCGTSA
YHCLMGSSESEMCFLSFLVPRPMTYTRGDLYNHVVPRPHNKRVPILPFVIRAGVLGRLG
TGGSITTSTQFYYKLSOEINGDMEGVTDSLYLQUGDLNSLAAVLQNRRADHILPF
RGGTCLFLGEBERCYVVNQSRITYTRGDLYDLYDLYDCNSLAAVLQNRRADHILPF
RGGTCLFLGEBERCYVVNQSRITYTRGDLYDLYDCNSLAAVLGNRRADHILPF
FLGFLABERTSTQFYRRAVKETRDRIQCRAEELQNTERWGLLSQWMPWTLPF
FLGFLABERTSTQFYVNGSRITYTRGDLYDRAGNSSNTKIYRGPLDR
PARLCSDVNDIEVTPPEEISTAQPLLHSNSVGSS"
                                                                                                                                                                                                                                                                                                                                                                                            /function="displaying superantigen-like properties causing polyclonal activation of human Vbeta 16 T-cells (CD3+) independent from the T-cell receptor antigen specificity" /note="surface and transmembrane regions"
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Camelo,S., Dumon,A., Jolivet-Reynaud,C., Marcel,F., Souillet,Y., Barch,E., Gabuhrer,L., Santoro,L., Marcel,S., Seigneurin,J.M., Marche,P.N. and Lafon,M. Multiple sclerosis retrovirus particles and recombinant envelope trigger an abnormal immune response in vitro, by inducing polyclonal Wbetal6 T-lymphocyte activation Virology 287 (2), 321-332 (2001)
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Perron, H., Ounanian-Paraz, A., Marcel, F. and Souillet, Y.
Direct Submission
Submitted (21-DEC-2000) R&D, bioMerieux, Chemin de L'Orme,
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99.2%; Pred. No. 0;
:ive 0; Mismatches
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/db_xref="taxon:89382"
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Location/Qualifiers
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1 (Sess 1 to 1629)
Perron, H., Jouvin-Marche, E., Michel, M., Ounanian-Paraz, A.,
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Signature, B., (Dates 1.0.) Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkiy, L., Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkiy, L., Anderson, S., Brown, A., Burkett, G., Campopiano, A., Castle, A., Changolo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M., Farnetra, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Grama, L., Horton, L., Hayland, J., Landers, T., Largocque, K., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R., McKernan, K., McPheeters, R., McIarim, J., Mandonal, P., Marquis, N., McCarnh, M., McKernan, K., McPheeters, R., McIarim, J., Mandova, T., Moron, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Taskaye, S., Theodore, J., Tirrell, A., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M. Direct Submission
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Homo sapiens clone RP11-15N10, WORKING DRAFT SEQUENCE, 33 unordered
                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. [1 (bases 1 to 17918)]
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo, sapiens, clone RP11-15N10
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1441 GAAGCTGTAAAGCTACAAATAGTTCTTCAAATGGAACCCCA 1481
                                                                                                                                                                                                     AC023366.2 GI:7143443
HTG: HTGS PHASB1; HTGS DRAFT.
HOMO SEDIENS (human)
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                                                                                                            CAAAACCCTACTAACTGTTGGATGTGCCTCCCCTGCACTTCAGGCCATACATTTCAATC
                                                                                                                                                                                                                                                                              CAAAACCCTACTAACTGTGGATGTGCCTCCCCCTGCACTTCAGGCCATACATTTCAATC
                                                                                                                                                                                                                                                                                                                                     CCTGTTCCTGAACAATGGAACAACTTCAGCACAGAAATAAACACCACTTCCGTTTTAGTA
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                                                                                       AGCACCCCTAGCCCCTACAAAGGACTAGTTCTCTCAAAACTACATGAAACCCTCCGTACC
                                                                                                                                                                     CATACTCGCCTGGTGAGCCTATTTAATACCACCCTCACTCGGCTCCATGAGGTCTCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                    GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACCTCACCTGTGTAAAATTT
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contig of 19285 bp in length
gap of 100 bp
contig of 18026 bp in length
gap of 100 bp
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contig of 22172 bp in length
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of 2277 bp in length
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Location/Qualifiers
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/mol_type="genomic DNA"
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FEATURES source

ö 1 AIGGCCCTCCCTTATCATACTTTCTCTTACCGTTCTCTTACCCCCTTTCGCTCTCACT Gaps DB 2; Length 172918; ; 12; Indels /clone="RP11-15N10" |Clone_11b="RPC1-11 Human Male BAC" | 1. 1266 | note="assembly_fragment" 98.7%; Score 1461.8; 99.2%; Pred. No. 0; iive 0; Mismatches 63499. 69283 /note="assembly_fragment" 69384. 75177 /note="assembly_fragment" 75278. 80817 8361. .42757 note="assembly_fragment" 2858. .46232 note="assembly_fragment" 46333. .51049 //note="assembly_fragment" 51150. .53373 /note="assembly_fragment" 58271. .63398 note="assembly_fragment" note="assembly_fragment" 7725. .30780 note="assembly_fragment" 4354. 38260 note="assembly_fragment" 2104. .14038 'note="assembly_fragment" note="assembly_fragment" 6327. .19115 9216. 21492 note="assembly_fragment" 1593. .24794 note="assembly_fragment" note="assembly_fragment" note="assembly_fragment" note="assembly_fragment" 4389. .5572 /note="assembly_fragment" .673. .6812 'note="assembly_fragment" note="assembly_fragment" note="assembly_fragment" 1150. .53373 note="assembly_fragment 2787. .4288 /note="aggembly_fragment" 1367. .2686 /note="assembly_fragment" 5913. .7404 /note="agsembly_fragment _xref="taxon:9606" rector_side:right" side:right" end:SP6 0881. .34253 clone_end:T7 Query Match 98.7 Best Local Similarity 99.2 Matches 1469; Conservative misc_feature 유 à d ò

	RESULT 11 AX478550 LOCUS LOCUS LOCUS Sequence 4 from Patent W00248362. ACCESSION AX478550 VERSION VERSION VERSION VERSION AM478550.1 GI:22217319 KEYWORDS SOURCE Homo sapiens (human) ORGANISM Hemo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	REFERENCE AUTHORS Ramkumar,J. and Arvizu,C. TITLE Embryogenesis associated proteins JOURNAL Patent: WO 0248365-A 4 20-JUN-2002; JOCATION/QUALIFIES LOCATION/QUALIFIES 1. 2074 / Organism="Homo sapiens" / Mol Lype="unassigned DNA" / Ab xref="taxon:9606" / Ab xref="taxon:9606" / NoTesting to No: 7477736CBI"	Query Match 93.8%; Score 1389.8; DB 6; Length 2074; Best Local Similarity 96.2%; Pred. No. 0; 0.0 Matches 1424; Conservative 0; Mismatches 57; Indels 0; Gaps 0; 0.0 Qy 1 ATGGCCCTCCCTTATCATATCTTATCTTATCTTATCTCTTACCCCTTTCACT 60 Db 64 ATGGCCCTCCCTTATTGTATTTTCTCTTTACTGTTCTCTCACCCTTTCAGTCTCACT 123	Qy 61 GCACCCCTCCATGCTGCTACAACCAGTAGCTCCCCTTACCAAGAGTTTCTATGAAGA 120 Db 124 GCACCCTCTCCATGCCACTGTAGGACCAGTAGCTCCCTTACCAAGCGTTTCTATGGAGA 183 Qy 121 ACGCGGCTTCCTGGAATATTGATGCCCCATCATATAGGAGTTTATCTAAGGGAAACTCC 180 Db 184 ATGCGGCTCCCAGACATATTGATGCCCCATCGTATAGGAGTTTATCTAAGGAAACCCC 243	Oy 181 ACCTTCACTGCCACACCCATATGCCCGCAACTGCTATAACTCTGCCACTCTTGCATG 240	QY 301 GGAGCCACTGTCTGTTGACTTCACCCATACCAGTGGAGGTGGAGTTGAATT 360 Db
121 ACGCGGCTTCCTGGAAATATTGATGCCCCATCATATAGGAGTTTATCTAAGGGAAACTCC 180	103654 AGCACCCCTAGAAAGGACTAGTTCTCTCAAAACTACATGAAACCCTCCGTACC	601 103834 661 103894 721	Qy 781 ATAGTCTGCCTACCCTCAGGAATATTTTTTGTCTGTGGTACCTCAGCCTATCATTGTTTG 840 Db 104014 ATAGTCTGCCTACCCTCAGGAATATTTTTTGTCTGTGGTACCTCAGCCTATCATTGTTTG 104073 Qy 841 AATGGCTCTTCAGAATCTATGTGCTTCCTCTCTATTGTGGCCCCCTATGACCATCTAC 900 Db 104074 AATGGCTCTTCAGAATCTATGTGCTTCCTCTCATTGTTGTGCCCCTATGACCATCTAC 1011111111111111111111111111111111111	Qy 901 ACTGAACAAGATTTATACAATCATGTGGTACCTAAGCCCCACAACAACAAGAGTACCCATT 960 Db 104134 ACTGAACAAGATTTATACAATCATGTGGTACCTAAGCCCCACAACAACAAAGAGTACCCATT 104193 Qy 961 CTTCCTTTTGTTATCAGAGCAGGAGTGCTAGGCAGACTAGGTACTGGCATTGGCAGTATC 1020 Db 104194 CTTCCTTTTGTTATCAAAGCAGGAGTGCTAGGCAGACTAGGTACTGGCATTGGCAGTATC 104253	Oy 1021 ACAACCTCTACTCTACTACTACAAACTATCTCAAGAAATAAAT	OY 1141 CAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTA 1200

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                                                                              PRI 11-FEB-2004
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
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                                                   10230 bp DNA linear PRI 11-FE. Gorilla gorilla isolate 1 endogenous retrovirus ERV-W, ERVWE1 locus, allele B, complete sequence. AY101589 AY101589.1 GI:37544413
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The endogenous retroviral locus ERVWE1 is a bona fide gene: In hominoid placental physiology proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004) 14757826
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90.6%; Score 1341.8;

Best Local Similarity 94.1%; Pred. No. 0;

Matches 1394; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                      The RPCI-43 BAC Library has been constructed by Chung-Li Shu. DNA was isolated from white blood cells obtained from a male chimpanzee (Pan troglodytes, Clint', Yerkes #C0471, birthdates = 6-6-80). The clone and detailed information can be obtained from ResGen (http://www.resgen.com) or Pieter de Jong and co-workers at http://www.bacpac.chori.org.
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                                                               This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality date (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
entire insert of this
    NOTICE: This sequence may not represent the entire insert of this close. I may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between naighboring data submissions.
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                                                                                                                                                                               MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence,
http://genome.wustl.edu
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This sequence is the entire insert of
Location/Qualifiers
1. 184675
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Pan troglodytes"
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/db_xref="taxon:9598"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Sequence derived
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/clone_lib="RPCI-43"
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                                          AGCACCCCTAGCCCCTACAAAGGACTAGTTCTCTCAAAACTACATGAAACCCTCCGTACC
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CAAGGTCAGGCAAGAGAAAAACAAGTAAAGGAAGCAATCTCCCAACTGACCCGGGGACAT
                                                                                   CATACTCGCCTGGTGAGCCTATTTAATACCACCTCACTCGGCTCCATGAGGTCTCAGGC
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/product="envelope glycoprotein"
/protein_id="AAM68165.1"
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/predmyFTHTGMRGGGVQDQAREKHVKEVISQLTRYHTTSV
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YRCLNGSSESMCFLSFLVPPMTIYTEODLYNYVVSKRRNRRVPILPFVIGAGVLGALG
TGGGTTTSTOPYYKLSGELNGDMERVADSLVTLQDQLNSLAAVVLQNRRALDLLTAE
RGGTCLFLGEECTYVNOSGTYPEKVKEIRDRIQRRAEELRATGPWGLLSQNWPWILP
FLGPLAAIILLLFGPCIFNLLVNFVSSRIEAVKLQMEPKMQSKTKIYRRPLDRPASP
                                                                                                                                                                                                                                                                                                                                             involved
                                                                                                                         PRI 11-FEB-2004
                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan. I (bases I to 10229)
Maller, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G., Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
The endogenous retroviral locus ERVWEI is a bona fide gene involve in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gag-pol pseudogene"
                                                                                                  10229 bp DNA linear PRI 11-FE Pan troglodytes isolate 1 endogenous retrovirus ERV-W, ERVWEl locus, allele A, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coding region"
                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 10229)
Maller,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (06-MAY-2002) Retrovirology Department, UMR 2142
CNRS-bioMeriaux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 6934 cedex 07, France
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /isolation source="PBMC of chimpanzee 1"
/db xref="taxon:9598"
/cell_type="PBMC"
/note="isolated by PCR; ERVWE1 locus, allele edogenous_virus: ERV-W"
                        155063 GAAGCTGTAAAACTACAAATGGAGCCCAAGATGCAGTCCAA 155103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(248. 810,2889. 9820)
join(248. 810,2889. 9820)
join(248. 810,7592. 9820)
/product="envelope glycoprotein"
/note="putative mRNA transcript 2"
join(248. 810,9255. 9820)
/note="putative mRNA transcript 2"
join(248. 810,9255. 9820)
/note="putative mRNA transcript 3; no co-
       1481
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        GAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAACCCCA
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Pred. No. 0;
0; Mismatches

    10229
    /organism="Pan troglodytes"
/mol_type="genomic DNA"
/isolate="1"

                                                                                                                                                                                                                           Pan troglodytes (chimpanzee)
Pan troglodytes
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Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 10229)
Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucottee,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWEL is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
                                                                                                                                                                                                                                                                                                                                       10229 bp DNA linear PRI 11-FEB-2004 Pan troglodytes isolate 1 endogenous retrovirus BRV-W, ERVWE1 locus, allele B, complete sequence.
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                                                                                                                 CTCAGCCAATGGATGCCCTGGGTTCTCCCCTTTAGGACCTCTAGCAGCTCTAATATTG
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              ATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAAAACACCGGAACGCTGGGGCCTC
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Direct Submission.
Submitted (OG-MAY-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69364 cedex 07, France
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/cell_type="PBMC"
/note="isolated by PCR; ERVWE1 locus, allele
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TYCWTYFTHTGWSDGGGYQUQAREKHYKEVISQLTRCHFAARRPYGLDLSKLHFTLRT
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7925
Hylobates pileatus (pileated gibbon)

Hylobates pileatus

Eukaryotas pileatus

Eukaryotas metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.

1 (Bases I to 10246)

Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G.,

Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.

The endogenous retroviral locus ERVWEl is a bona fide gene involved in hominoid placental physiology

Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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/db_xref="taxon:9589"
/cell_type="PBMC"
/note="isolated by PCR; ERVWE1 locus, allele-endogenous_virus: ERV-W"
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (OG-MAY-2002) Retrovirology Department,
Submitted (OG-MAY-2002) Retrovirology Department,
GNRS-bioMerieux, Ecole Normale Superieure de Lyon
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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join(248. .254,2843. .9807)

/note="putative mRNA transcript 1; gav

join(248. .254,7579. .9807)

/product="envelope glyroprotein"

/note="putative mRNA transcript 2"

join(248. .254,9242. .9807)

/note="putative mRNA transcript 3; no
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/mol type="genomic DNA"
/isolate="1"
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 alle
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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/mol type="genomic DNA"
/molare="individual 132 allele
/db.xref="taxon:9606"
/chromosome="7"
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/sex="female"
/cell_type="PBMC's
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Pred. No. 0;
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Best Local Similarity 94.0%;
Matches 1392; Conservative (
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AF520487S2 2694 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 148 allele B, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence. AF52048B
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Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G., Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
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endogenous_virus: HERV-W"
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/rodon_start=1
/product="envelope glycoprotein"
/protein_id="AAQ17561.1"
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90.2%; Score 1335.4;
Best Local Similarity 93.9%; Pred. No. 0;
Matches 1390; Conservative 0; Mismatches
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/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="ladvidual 148 allele B"

/db_xref="taxon:9606"

/chromosome="7"

/map="7421-422"

/cell_type="PBMC's"

/cell_type="PBMC's"
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 2694)

Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,

Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.

The endogenous retroviral locus ERVWEl is a bona fide gene involved in hominoid placental physiology

Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
                                                                                                              AF520489S2 2694 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 22 allele A, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mallet, F., Bouton, O. and Oriol, G.
Direct Submission

Direct Submission

CNRS-bioMerieux, Bcole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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Pred. No. 0;
0; Mismatches
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.959. .2694
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Homo sapiens (human)
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Best Local Similarity 93.9
Matches 1390; Conservative
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KEYWORDS
SEGMENT
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ORGANISM
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REFERENCE
AUTHORS
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Length 2694;

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us-09-319-156b-9.rge

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YRCLNGSSEBMCFLSFLVPPWT1YTEQDLYNYVISKPRNKRVPILPFVIGAGVLGALG
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LVGPLVSNLEITHTSNLTCVKFSNTTYTTNSQCIRWVTPPTQIVCLPSGIFFVCGTSA
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                                                                           RSDVNDIKGTPPEEISAAQPLLRPNSAGSS"
1705. 1720
//note="splice acceptor site"
1959. 2694
                                                                                                                                                                            Score 1335.4;
Pred. No. 0;
0; Mismatches
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2694 bp

DNA

linear

PRI 11-FEB-2004

Homo sapiens individual 37 allele A, envelope glycoprotein gene,
complete cds, and 3' long terminal repeat, complete sequence.

AF520506

AF520506.1

GI:33410980
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The endogenous retroviral locus ERVWE1 is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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1664 CTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAACTTTTTCCAGAATC 1723
                                                                                                                                                                                                                 CTCAGCCAATGGATGCCCTGGATTCTCCCCTTTTAGGACCTCTAGCAGCTATAATATTG 1663
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   CTCAGCCAATGGATGCCCTGGGTTCTCCCCTTTTAGGACCTCTAGGACTCTAATATTG
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- 46 allee
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Direct Submission
Submitted (O'JUN-2002) Retrovirology Department,
CNRS-bioMerieux, Ecole Normale Superieure de Lyon
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/note="endogenous_virus: HERV-W"
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/note="syncytin"
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                                               /"Sex="female"
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/note="endogenous_virus: HERV-W"
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/chromosome="7"
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1959. .2694
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Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWE1 is a bona fide gene involved
in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                           CTTCCTTTTGTTATCAGAGCAGGAGTGCTAGGCAGACTAGGTACTGGCCATTGGCAGTATC
                                                                                                                            Mallet, F., Bouton, O., and Oriol, G.
Direct Submission
Submitted (OrJUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 63934 cedex 07, France
Location/Qualifiers
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    2694
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                                                          Mallet, F. Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G., Mallet, F., Bouton, O., Duret, L. and Mandrand, B.

Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.

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Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mallet,F., Bouton,O. and Oriol,G.
Mallet,F., Bouton,O.
Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMeritux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 6934 cedex 07, France
Location/Qualifiers
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/note="endogenous_virus: HERV-W"
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                                                                                                          GGACCTCTTGTTTCCAATCTGGAATAACCCATACCTCAAACCTCACCTGTGTAAAATTT
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1 (bases 1 to 2694)
Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWEl is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
                                                                                                                                                                                                    AF520521S2 2694 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 6 allele A, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
1664 CTACTCCTCTTGGACCCCTGTATCTTTAACCTCCTTGTTAACTTTGTCTCTTCCAGAATC 1723
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Direct Submission
Submitted (OrJUN-2002) Retrovirology Department,
CNRS-bioMerieux, Ecole Normale Superieure de Lyon
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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/isolate="individual 6 c/db xref="taxon:9606"
/chromosome="7"
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/note="syncytin"
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Best Local Similarity 93.9%; Pred. No. 0;
Matches 1390; Conservative 0; Mismatches
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AF208161.1 GI:6760400
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/ CASTEF="GI-18620524"
/ LEANSIALION="WALPHYHIELFIYILPSFTLITAPPPCRCWTSSSPYGEFLWRMQRPGNIDAPSYRSISKGTPFTAHTHWPRNCYHSATLCWHANTHYWTGKMINPSCPGGLGVTVCWTYPTOTGMSDGGGVQNQAREKHYKEVISQLINFRYVGISPYKGLDISKLHFTLRTHTRUSLENTTTTGLHEVSENTYTTNGCITRWTPPTQTVCTCLPSGIFTRY
HTRLVSLENTTTGHLEVGKESNTTYTTNGCITRWTPPTQTVCLPSGIFFVCGTSA
INCLNGSSESMCFLSFLVPPWT1YTTGQLYNYVISKPWTRVPILPFVIGAGVLGALG
TGTGGITTSTQFYXLSQELMGDMERVADSLYTLQDQLNSLAAVYLQNRRALDILTAE
RGGTCLFLGEECCYYVNQSGIVTEKVKEIRDRIQRRAEBELRNTGPWGLLSQWMWILLP
FLGFLAAIILLLFGPCIFFILLVNFVSSRIEAVKLQWEPKMQSKTKIYRRPLDRPASP
RSDVNDIKGTPPEEISAAQPLLRPNSAGSS"
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                                             Craniata; Vertebrata; Euteleostomi;
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Pred. No. 0;
0; Mismatches 91; Indels 0;
                                                                                                  treating
                                                                                                and
                                                                                                                                                               Keith, J.C., Mccoy, J.M. and Mi, S.
Methods and compositions for diagnosing
and gestational trophoblast disorders
Patent: WO 0204678-A 1 J7-JAN-2002;
GENETICS INSTITUTE, INC. (US)
                 Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa, Chordata, (
Mammalia, Eutheria, Primates, (
                                                                                                                                                    Location/Qualifiers
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                                                  ACCTICACTGCCCACACCATAIGCCCCGCAACTGCTATAACTCTGCCACTCTTTGCATG 240
ATGCAGCGTCCCGGAAATATTGATGCCCCATCGTATAGGAGTCTTTCTAAGGGAACCCCC 1109
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| note="envelope protein"
| codon start="envelope protein"
| codon start="envelope protein"
| product="syncytin precursor"|
| protein_id="AAF28334.1"
| protein_id="AAF28334.1"
| protein_id="AAF28334.1"
| db xref="G1:6760401"
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E 1 (Dases 1 to 2946)

S Jacobs, K., Mccoy, J.M., Lavallie, E.R., Racie, L.A.C., Evans, C., Merberg, D., Mi, S. and Treacy, M.

Secreted proteins and polymucleotides encoding them Secreted proteins and polymucleotides encoding them Secreted proteins and polymucleotides encoding them Secreted proteins and polymucleotides encoding them Secreted proteins and polymucleotides Practice INSTITUTE INC

OS Homo sapiens (human)

PN 12 2002515234-A/2

PD 28-MAY-2002

PF 17-MAY-1999 JP 2000549638

PR 18-MAY-1999 JP 2000549638

PR 18-MAY-1999 US 09/080478, 20-OCT-1998 US 09/175928 PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A COLLINS PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A COLLINS PI CHENYL EVANS, DAVID MERBERG, SHA MI, MAURICE TREACY PC CI2NIS/09, A6IR38/00, A6IR45/00, A6IR48/00, A6IR48/00, A6IR49/00, A6IR49/00, AGIR493/00, AGIR38/00, A6IR93/00, COTKI4/47, CI2NIS/10, CI2P21/02, PC AGIR38/00, A6IR93/00, AGIR493/00, COTKI4/47, CI2NIS/10, CI2P21/02, PC
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The HERV.W/7q family in the human genome. Potential for protein expression and gene regulation cell. Mol. Biol. 48, 213-217 (2002)

Goldou, D., Perin,J.P., Rieger,F., Robert,B. and Alliel,P.M. Direct Submission

Submitted (29-ARF.2002) U-488, INSERM, 80, rue du General Leclerc, Le Kremlin-Bicetre 94270; France

Location/Qualifiers
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Alliel.P.M., Perin.J.P., Goudou,D., Bitoun,M., Robert,B. and
                                                                                                         Endogenous retroviruses and multiple sclerosis. II. HERV-7q C. R. Acad. Sci. III, Sci. Vie 321 (10), 857-863 (1998) 99052087
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Alliel, P.M., Goudou, D., Perin, J.P. and Rieger, F.
Submitted (18-MAY-2002) U-488, INSERM, 80, rue du General Leclerc,
Le Kremlin-Bicetre 94270, France
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C. R. Acad. Sci. III, Sci. Vie 312, 857-863 (1998)
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Alliel, P.M., Perin, J.P., Goudou, D., Bitoun, M., Robert, B. and Rieger, F.
The HRN-W/7q family in the human genome. Potential for protein expression and gene regulation
Cell Mol. Biol. 48 (2), 213-217 (2002)
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ò	1201	GGAGAAGAACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAA 1260	09:	
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q	1544	ATTCGAGATCGAATACAACGTAGAGCAGAGGAGCTTCGAAACACTGGACCCTGGGGCCTC 1603	103	
ò	1321	CTCAGCCAATGGATGCCCTGGGTTCTCCCCTTTAGGACCTCTAGGAGCTCTAATATTG 138	1380	
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ò	1381	TTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTTGTCTCTTCCAGAATT 1440	140	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
-	1481	0.001	1481		AAV43217	Aav43217 Multiple
	1481	100	1481	· ~	AAX29703	Aax29703 Clone C15
- 1	1481	100.0	1481	12	ADG14846	Adq14846 MSRV asso
4	1481	100.0	2030	'n	AAA63826	Aaa63826 Nucleotid
	1461.8	98.7	1629	m	AAA96625	Aaa96625 DNA encod
9	1450	97.9	1481	6	ADB84400	Adb84400 MSRV-1 as
7	1389.8	93.8	2074	9	AAD41225	Aad41225 Human EMB
- 00	1335.4	90.2	2930	9	AAD24195	Aad24195 Human syn
o	1335.4	90.2	2946	N	AAX77526	Aax77526 Human sec
10	1335.4	90.2	2946	m	AAZ59468	Aaz59468 Human sec
11	1335.4	90.2	2946	10	ADC38776	Adc38776 Human cDN
12	1333.8	90.1	1617	ഗ	AAH20070	Aah20070 HERV-W en
۳ ا	1333.8	90.1	2055	m	ABN97948	Abn97948 Human ret
14	1333.8	90.1	2599	٣	ABN97927	Abn97927 Human ret
15	1333.8	90.1	8523	7	ADS30988	Ads30988 Human gen
16	1333.8	90.1	10499	ო	ABN97929	_
17	1333.8	90.1	56093	9	ABL61744	
18	1330.6	89.8	2781	S	AAF55630	. Aaf55630 Nucleotid
13	1324.2	89.4	7582	m	AAA59215	Aaa59215 Human end
20	1322.6	89.3	7582	~	AAX25665	Aax25665 Complete

2 2782 5 AAH20069 2 2782 3 AAX25661 2 2782 3 AAX25661 3 464 10 ADE59587 3 464 10 ADE59718 3 16334 11 ACM44334 4 ABA58778 4 1894 4 ABA5837 4 1894 4 ABA5837 4 1894 4 ABA5878 4 1894 4 ABA5878 4 1894 4 ABA5878 4 1894 4 ABA5878 4 1894 4 ABA5878 4 1894 4 ABA5878 4 1894 4 ABA5878 4 1894 4 ABA5878 4 1894 5 AAX3688 4 1894 6 ABA5878 4 1894 6 ABA5878 4 1894 6 ABA5878 4 1894 6 ABA5878 4 1894 6 ABA5878 4 1894 6 ABA5878 4 1894 6 ABA5878 4 1894 6 ABA5878 4 1894 6 ABA5878 6 ABA68919 AAX3889 AAX3889 AAX3889 AAX3889 AAX3889 AAX3889 AAX3889 AAX3889 AAX3889 AAX3889 AAX3889 AAX3889 AAX38888 AAX3888	ALIGNMENTS ard; cDNA; 1481 BP. Lirst entry) sais associated retrovirus fragment 5.	natoid arthritis-associated virus; MSRV; MS; pol gene; gag gene; natoid arthritis-associated virus; ss. Dostion/Qualifiers Location/Qualifiers /*tag= a /*tag= a /product= "Encodes protein AAW71068" /ransl_except= (pos:115-117, appears to code for a stop codon) /note= "CDS does not contain a stop codon"	97WO-IB0014&2. 96US-00756429. MERIEUX.	eme F, Bedin F, ParanhoB-Baccala G; 1 F, Jolivet-Reynaud C, Mandrand B; 32/28. 68. id from retroviruses - useful for diagnosis, prevention and e.g. multiple sclerosis. ge 184-185; 286pp; English.
8 8 8 8 8 8 8 8 8 8 8 8 8 6 6 6 6 6 6 6	tanda 8 (f	cleros	A1. 8. 7; 9 6; 9 MERI	Besemadel 22732 71068 acid f, e.
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    The present sequence represents a multiple sclerosis (MS) associated retrovirus (MSRV) genomic fragment used in the method of the invention. The invention provides complete or partial genomic sequences of the MSRV-1 pol gene, gag gene and env gene, and polypeptides encoded by these genes. The invention also provides antibodies raised against the polypeptides. The genomic sequences, polypeptides and antibodies are also claimed useful for diagnosing infection by MS and rheumatoid arthritis-associated viruses, and also for prevention and treatment of infection with these viruses
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                                                                               This sequence represents clone C15 from a novel multiple sclerosis related virus type 1 (MSRV1). The sequence can be used in diagnostic, prophylactic or therapeutic compositions to inhibit expression of a multiple sclerosis related virus and/or virus associated with rheumatoid polyarthritis. (Updated on 27-ANGS-2003 to correct OS field.) (Updated on 17-OCT-2003 to standardise OS field)
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                           Nucleic acid sequences of retrovirus called MSRV-1 - associated with multiple sclerosis or rheumatoid polyarthritis.
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                                                                                                                          The invention relates to an isolated nucleic acid which comprises the gene of a retrovirus associated with multiple sclerosis or rheumatoid arthitis. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating multiple sclerosis and/or rheumatoid arthitis. The present sequence is used in the exemplification of the invention.
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                                                           New isolated nucleic acid and their fragments retrovirus, useful for diagnosing, preventing sclerosis and/or rheumatoid arthritis.
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CAAGGTCAGGCAAGAAAAAAAGTAAAGGAAGCAATCTCCCAACTGACCGGGGGACAT
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                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents the nucleotide sequence corresponding to the 3' env region and long terminal repeat sequences from clone CL6 of MNILiple Sclerosis retrovirus (MSRV-1). The specification describes a long terminal repeat (LTR)-RUS region which encodes the expression of a MSRV-1 protein. This is unusual for LTRs, in particular in the RUS region. The sequence includes CAAT and TARA signals which are present in the features table. Probes and artibodies to the MSRV-1 retrovirus to the in and encoding polynucleotide sequences are used to detect the presence of MSRV-1 retrovirus in a biological sample. (Updated on 06-AUG-2003 to correct OS field.)
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100.0%; Pred. No. 0;
ive 0; Mismatches
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1906. 1911
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P-PSDB; AAB08195.
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Matches 1481; Conserv
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                                                             GGAGCCACTGTCTGTTGGACTTACTTCACCCATACCAGTATGTCTGATGGGGGTGGAATT
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                                                                                                                                                                                           Envelope protein; MSRV-1; superantigen; autoimmune disease; Vbetal6;
Vbetal7; multiple sclerosis; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting superantigen activity, useful for identifying agents for treatment or prevention of autoimmune disease, from expansion or luparticular lymphocyte Vbeta determinants.
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Pred. No. 0;
0; Mismatches 12; Indels
an envelope (env) protein of MSRV-1
                                                                                                                                                                                                                                                              Location/Qualifiers
1. .1629
/*tag= a
/product= "envelope protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; Page 123-124; 134pp; French
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Best Local Similarity 99.2%;
Matches 1469; Conservative 0
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99FR-00013755
                                                                                  AAA96625 standard; DNA; 1629
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                                                                                                                                                                                                                                     Human endogenous retrovirus
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P-PSDB; AAB19069.
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28-OCT-1999;
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primer for the amplification by polymerisation of a nucleic acid of a viral material associated with multiple sclerosis or rheumatoid archivitis, a polypeptide exhibiting an inhibitory activity on the proteolytic, reverse transcriptes or ribonuclease H activity from MSRV, and an antibody directed against the MSRV-1 virus obtained by immunologically reacting a human or animal body or cells with an immunogenic agent consisting of the antiganic polypeptide defined above. The nucleic acids are useful for detecting a biological sample a virus associated with multiple sclerosis or rheumatoid arthritis, or for associated with multiple sclerosis or rheumatoid arthritis. Or for associated with multiple sclerosis or rheumatoid arthritis. The present sequence is a claimed MSRV-associated sequence whose identity cannot be accurately determined. Note: The SEQ ID numbers for the sequences as displayed in the main body of the patent do not match the SEQ ID numbers in the sequence listing. Consequently those sequences mentioned in the
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and mucleic acid molecules encoding such proteins. EMBRY sequences are useful for screening modulators useful for treating or preventing disorders associated with abnormal expression of EMBRY. The disorders treated include reproductive disorders such as infertility, endometriosis, endometrial or ovarian tumour; autoimmune/inflammatory endometriosis, endometrial or ovarian tumour; autoimmune/inflammatory contact dermatitis; disorders of the placenta such as preeclampsia, abruptic placentes etc. Sequences of the invention are also useful for analysing a proteome of a tissue or a cell type. EMBRY proteins are useful as immunogens for preparing antibodies. Polynucleotides of the invention are useful for creating knockin humanised animals or transgenic animals to model human diseases. They are also used in gene therapy. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ACGCGGCTTCCTGGAAATATTGATGCCCCATCATATAGGAGTTTATCTAAGGGAAACTCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptides of human embryogenesis associated proteins for screening modulators useful for treating or preventing disorders e.g. endometriosis, infertility, allergy, preeclampsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 ATGGCCCTTATTGTATTTTTCTCTTTACTGTTCTCTCACCACCTTTCAGTCTCACT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to human embryogenesis associated proteins (EMBRY)
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                                                                                                               "Mature EMBRY-2 protein'
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Pred. No. 0;
0; Mismatches
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96.2%;
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Matches 1424; Conservative
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Best Local Similarity
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The invention relates to identifying compounds which are modulators of syncytin expression. The syncytin modulators are useful in diagnosis and treatment of preeclampsia and gestational trophoblast disorders (e.g. choriocarcinoma, hydatiform mole, placental site tumour and missed, incomplete abortion). Syncytin is a human gene derived from the envelope gene of human endogenous defective retrovitus, HRRV-W. The present invention is based partly on the discovery that syncytin expression is dramatically reduced in preeclampsia, and is also mis-localised to the apical syncytiotrophoblast membrane. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying a compound for treating a subject with or at risk of developing preeclampsia, comprises determining whether the expression or activity of syncytin in the cell is modulated in the presence of a test
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1504 GAAGCTGTAAAGCTACAAATGGTTCTTCAAATGGAGCCCCA 1544
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Pred. No. 0;
0; Mismatches
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/product= "Syncytin"
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930. .2546
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                                                                 AAD24195 standard; cDNA; 2930
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nilarity 93.9%;
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                                                                                                                                              Human syncytin cDNA.
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Best Local Similarity
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This invention describes novel human secreted proteins encoded by polynucleotides isolated from human adult testes, adult brain, adult blood or adult placenta, or murine adult bone marrow or thymus cDNA libraries. The products of the invention are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, haemacopoiesis regulating activity, tissue growth activity, and activity, chemoatopoiesis regulating activity, tissue growth activity, and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotides are also stated to be useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                 Secreted protein; testes; brain; blood; placenta; human; murine; thymus; bone marrow; treatment; prevention; nutrition; cytokine; immune; vaccine; cell proliferation; cell differentiation; suppressor; tumour inhibition; haematopoiesis regulator; activin; inhibit; chemotactic; chemokinetic; haemostatic; thrombolytic; receptor; ligand; anti-inflammatory; tumour; cadherin; tumour invasion suppressor; gene therapy; tissue growth; ss.
                                                                                        ATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAAAACACCGGAACGCTGGGGCCTC
                               2190 ATTCGAGATCGAATACAACGTAGAGCAGAGGACTTCGAAACACTGGACCCTGGGGCCTC
                                                                       CTCAGCCAATGGATGCCCTGGGTTCTCCCCTTTAGGACCTCTAGCAGCTCTAATATTG
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98US-00080478.
98US-00175928.
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Treacy M;
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	RESULT 10, AAZ59468 standard; CDNA; 2946 BP. XX AZ59468; XX XX XX XX XX XX XX 11-APR-2000 (first entry) E Human secreted protein AJ172_2 polynucleotide sequence. XX XX XX XX XX XX XX XX XX
CC gene therapy X	0y 421 AGCACCCTAGCACACAAAGGACTAGTTCTCTCAAAACTACATGAAACCCTCCGTACC 480 1348 GGGACTCTAGCCCCTACAAAGGACTAGATCTCTCAAAACTACATGAAACCCTCCGTACC 1407 481 CATACTCGCCTACAAGACTAGATTAAAACCCTCCATGAGATCTCAGCC 540 1468 CATACTCGCCTACTAACTGTTGAATTAAAACCCTCCATGAGCTCCATGAGTCTCAGCC 1467 bb 1468 CATACTCGCCTACTAACTGTTGAATTAAAACCCTCCATGAGCTCCATGAGTCTCAGCC 1467 0y 601 CCTGTTCCTGAACATGTTGAATTAAAACCCTCCCCTCAACTTCAGCCATTTTAATC 1527 0y 601 CCTGTTCCTGAACAACTGTGGAACAACTTCAGCACTTCAGGCCATATTTTAATC 1527 0y 601 CCTGTTCCTGAACAACTGTGGAACAACTTCAGCACTTCAGGCCATATTTTAATC 1527 0y 61 GGACCTCTTGTTTCCAATCTGGAAATAACCCTCACACTTCAGGCCATTTTAATT 1647 0y 721 AGCAATACTAATAGAACAACTGGAAATAACCCAACTCCACTTCAGTTAAATTT 1647 0y 721 AGCAATACTAATAACAACTGGAAATAACCCAACTCCAACTCTCCACACAA 1707 0y 721 AGCAATACTAAAACACAACCAACAACAACAACAACTCCACCTCCCACACAA 1707 0y ATAGTCTGCCTCACAACTGGAAATAATTTTTTTTTTTTT

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                                                                                      This is the human secreted protein AJ172 2 nucleotide sequence, obtained from a human adult testes CDNA library. The invention relates to secreted human and murine proteins. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Detection of the levels of the proteins can be used for the diagnosis of e.g. pre-eclampsia, placental pathology or cancer. Agents which modulate the expression or function of the proteins may be used for treating a neoplastic disease and inhibiting metastasis. Other suggested activities include nutritional activity (e.g. in feeds), cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopoiesis regulating activity, itsue growth activity, activity, haematopoiesis regulating activity,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotide sequences are also stated to be useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATACTCGCCTGGTAAGCCTATTTAATACCACCCTCACTGGGCTCCATGAGGTCTCGGCC
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Best Local Similarity 93.9%; Pred. No. 0;
Matches 1390; Conservative 0; Mismatches 91; Tradale n.
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                                           Page 107-108; 149pp; English
                                           14;
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Gaps

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91; Indels

Mismatches

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61 GCACCCCCTCCATGCTGCTGTACAACCAGTAGCTCCCCTTACCAAGAGTTTCTATGAAGA

ATGGCCCTCCCTTATCATACTTTTCTCTTTACTCTTTACCCCCTTTCGCTCTCACT

1107

ACGCGGCTTCCTGGAAATATTGATGCCCCATCATATAGGAGTTTATCTAAGGGAAACTCC

240

300

360

ACCTICACTGCCCACACCCATATGCCCCGCAACTGCTATCACTCTGCCACTCTTTGCATG 1167

ACCTICACTGCCCACACCCATATGCCCCGCAACTGCTATAACTCTGCCACTCTTTGCATG

181 1108 1168

241

1228 361 1288

301

CATGCAAATACTCATTATTGGACAGGGAAAATGATTAATCCTAGTTGTCCTGGAGGACTT

GGAGTCACTGTTGGACTTACTTCACCCAAACTGGTATGTCTGATGGGGGGTGGAGTT 1287

CAAGGTCAGGCAAGAAAAAACAAGTAAAGGAAGCAATCTCCCCAACTGACCCGGGGACAT CAAGATCAGGCAAGAGAAAAACATGTAAAAGAAGTAATCTCCCAACTCACCCGGGTACAT

GGAGCCACTGTCTGGACTTACTTCACCCATACCAGTATGTCTGATGGGGGTGGAATT

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AGCACCCCTAGCCCCTACAAAGGACTAGTTCTTCTAAAACTACATGAAACCTCCGTACC

CAAAACCCTACTAACTGTTGGATGTGCCTCCCCTGCACTTCAGGCCATACATTTCAATC CCTGTTCCTGAACAACTGCACAACTTCAGCACAGAAATAAACACCACTTCCGTTTTAGTA

CATACTCGCCTGGTGAGCCTATTTAATACCACCTCACTCGGCTCCATGAGGTCTCAGCC

480

1467 540

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sequence represents cDNA encoding a human secreted protein.
                                                                                                                                                                                                        2946 BP; 858 A; 801
        Homo sapiens
                                                                                               Jacobs K, M
Merberg D,
Kelleher K;
                                                   1996;
                                                                        13-JAN-1997
                                                                                 05-SEP-1997
06-OCT-1999
                                          17-JUN-1996
                                                          SEP-1996
                                                                966
                   19-DEC-2002
                                    19-APR-1996
                                                                              32-JUN-1997
                                        07-JUN-1996
                                                      -SEP-1
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                                                                  -0CT-1
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Matches 1390; Conservative
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Croscominar proteins. The polynucleotides are useful for

Croscombinant proteins for analysis and are also useful so

chromosome markers or tags to identify chromosomes or to map related gene

chromosome markers or tags to identify chromosomes or to map related gene

chromosome markers or tags to identify chromosomes or to map related gene

continued. The proteins are useful as amino acid supplement, carbon

continued immunodeficiency (SCID)), autoimmune disorders (e.g. severe

combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple

continued immunodeficiency (SCID)), autoimmune disorders (e.g. multiple

continued immunodeficiency (SCID)), autoimmune disorders (e.g. multiple

coleropsis, systemic lupus erythematosus, rheumacoid arthritis), allergic

calerosis, systemic lupus erythematosus, rheumacoid siseases (e.g.

cosqulation disorders, inflammatory diseases (e.g. systemic inflammatory

cosqulation disorders, inflammatory diseases (e.g. systemic inflammatory

cresponse syndrome (SIRS), ischaemia-reperfusion injury, Crohn's disease),

conspubliaxis and hypersensitivity, Proteins are also useful for inducing

cumour immunity, for inducing bone, cartilage, tendon, ligament and/or

cregomerating nerve and brain tissue, for inducing fertility and for

cregomerating nerve and brain tissue, for inducing fertility and for

chibibiting tumour growth. Proteins are also useful as chemokine for

mammalian cells (e.g., monocytes, fibroblasts, neutrophils), and also

cuseful as inhibitors of receptor/ligand interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proteins AZ3021 encoded by clone AZ3021 from human adult colon, and BD12716 encoded by clone BD12716 from human fetal kidney cDNA library, useful for treating e.g. multiple sclerosis and rheumatoid arthritis.
hypersensitivity; regeneration; neural cell proliferation; fertility; tumour; chemokine; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Collins-Racie LA, Evans C;
Spaulding V, Carlin-Duckett M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 134; 412pp; English.
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Bowman MR,
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96US-00628364.
96US-00659221.
96US-00664936.
96US-0067431.
96US-007131.
96US-0072148.
96US-0072148.
96US-0072148.
96US-0072148.
96US-0072133.
96US-0073133.
96US-0073133.
96US-0073133.
96US-0073133.
96US-0073133.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEMY ) GENETICS INST INC
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Treacy M,
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P-PSDB; ADC38777.
                                                                                                                                                          US2002193567-A1
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1020 1080 1647 1767 1887 2007 1587 1707 1827 720 780 840 900 960 AATGGCTCTTCAGAATCTATGTGCTTCCTCATTCTTAGTGCCCCCTATGACCATCTAC GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACCTCTGTGTAAAATTT AGCAATACTATAGACACCAGCTCCCAATGCATCAGGTGGGTAACACCTCCCACAGA AGCAATACTACATACAACCAACTCCCAATGCATCAGGTGGGTAACTCCTCCCACACAA ATAGTCTGCCTACCCTCAGGAATATTTTTTGTCTGTGGTACCTCAGCCTATCATTGTTTG ATAGICTGCCTACCCTCAGGAATATITITGTCTGTGGTACCTCAGCCTATCGTTGTTTG AATGGCTCTTCAGAATCTATGTGCTTCCTCTATTCTTAGTGCCCCCTATGACCATCTAC ACTGAACAAGATTTATACAATCATGTCGTACCTAAGCCCCACAACAAAAGAGTACCCATT CTTCCTTTTGTTATCAGAGCAGGAGTGCTAGGCAGACTAGGTACTGGCATTGGCAGTATC 1948 ACAACCTCTACTCATTACTACTACAAACTATCTCAAAACTAAATGGGGACATGGAACGG GGACCTCTTGTTTCCAATCTGGAATAACCCATACCTCAAACCTCACTGTGTAAATTT 1648 1708 1828 1888 1021 1528 1588 721 661 781 841 1768 901 961 셤 g ઠે 유 8 원 8 d ð ò ద ð

Length 2946;

DB 10;

Score 1335.4; Pred. No. 0;

93.98;

Query Match Best Local Similarity

C; 570 G; 717 T; 0 U; 0 Other;

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cc endogenous retrovirus (HERVs) the full length endogenous provirus which was been located on the long arm of human chromosome 7 (7q21-22) has been designated HERV-W. The present invention describes proteins or peptides (1) having superantigen (SAQ) activity comprising the ENV protein (ENV) of HERV-W, the surface protein (SU) and transmembrane (TM) sub-units. (I) have neuroprotective activity, and can be used in: vaccines; antisensetherapy; and HERV-W SAQ activity-inhibitors. (I) and encoding DNA/RNA are useful for diagnoshing multiple sclerosis (MS) or HERV-W-associated disorders. (I) are also useful for identifying substances (and optionally crecovering) capable of binding to a retroviral superantigen associated with MS, substances capable of binding to a retroviral substances capable of binding to a retroviral substances capable of binding to a retroviral substances capable of binding to a retroviral substances capable of binding to a retroviral substance capable of blocking space of capable of blocking standing an immune response devoid of SAQ activity and being capable of generating an immune response capable of blocking sAQ activity, capable of binding to a retroviral capable of blocking transcription or translation of HERV-W retroviral superantigen for use in treating or translation of HERV-W retroviral superantigen for use in treating or prevention of MS. (I) and nucleic acids encoding them are useful for diagnosing autoimmune disease. The present sequence encodes the specifically claimed envelope protein of HERV-W designated G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GCACCCCCCCCCTCCATGCCGCTCTATGACCCGCTTACCCAGAGAGTTTCTATGGAGA 120
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                                                                                                                                                                                                                                                              Human endogenous retrovirus; HERV-W; HERV; chromosome 7; env protein; envelope protein; multiple sclerosis-related superantigen; vaccine; surface antigen; transmembrane; multiple sclerosis; neuroprotective; antisense-therapy; autoimmune disorder; ds.
                               GTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTT
                                                     GTCGCCGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGCAGTAGTTCTT
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The present invention relates to new mucleic acid sequences of human endogenouse retrovirus, HERV-7q, which is located on chromosome 7q. Regulatory elements associated with HERV-7q may alter expression of other genes (even remote genes) on the same chromosome, inducing immunological and/or neurological changes (which may be pathological or protective/curative). HERV-7q peptides can be used to improve efficiency of the immunor response, e.g. in immunofensay. HERV-7q peptides and their coding sequences can be used in immunogenic or vaccinating compositions, for protection against autoimmune diseases, particularly multiple sclerosis. The peptides may also be used (by sequence comparison) to detect/identify endogenous retroviruses that are abnormally expressed in cancer, neuropathologies or other autoimmune diseases. The present sequence was
                                                                                                                                                                               New nucleic acid sequences of human endogenous retrovirus, HERV-7q, use for diagnosis, treatment and prevention of autoimmune and neurological
                                                                                                                                                                                                                                    Claim 3; Page 142-145; 225pp; French.
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Sequence 2055 BP; 576 A; 574 C; 376 G; 529 T; 0 U; 0 Other;
                                                                                1 ATGGCCCTCCCTTATCATACTTTTCTCTTTACTGTTCTCTTACCCCCTT
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                            DB
                           Score 1333.8;
Pred. No. 0;
0; Mismatches
                            90.1%;
93.8%;
                                                       Conservative
                                          Best Local Similarity
Matches 1389; Conserv
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disease; HERV-7q; chromosome 7q; immunotherapy;

Human endogenous retrovirus

multiple sclerosis;

Autoimmune

Human retroviral HERV-7q env coding sequence

(first entry)

01-AUG-2002

ABN97948

ABN97948 standard; DNA; 2055

ABN97948

HERV-7q; chromosome 7q; immunotherapy;

g,

multiple sclerosis;

disease;

Autoimmune

Human endogenous retrovirus.

WO9967395-A1

29-DEC-1999,

sequence HERV 7

retroviral

Human

(first entry)

01-AUG-2002

(INRM) INSERM INST NAT SANTE & RECH MEDICALE.

99WO-FR001513 98FR-00007920

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RESULT 14 ABN9792' ABN97927

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Single copy genomic hybridization probes for detecting specific nucleic acid sequences in sample by in situ hybridization useful for detection of histone cell cycle regulation defective, S. cerevisiae homologue A; HIRA; high complexity repeat; in situ hybridisation; Southern blot; chromosome breakpoint; inherited genetic disease; neoplastic disorder; chromosome 22; DiGeorge syndrome; Velo-Cardio-facial syndrome. high complexity repeat found in the HIRA gene #21 1441 GAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAACCCCA 2369 GAAGCTGTAAAACTACAAATGGAGCCCAAGATGCAGTCCAA 14-MAY-2001; 2001US-00854867. 16-MAY-2000; 2000US-00573080. ADS30988 standard; DNA; 8523 (first entry) Knoll JHM, Rogan PK; (KNOL/) KNOLL J H M. (ROGA/) ROGAN P K. WPI; 2002-062378/08. US2003224356-A1. Homo sapiens. Human genome 18-NOV-2004 04-DEC-2003. ADS30988; 셤 ठ

acquired or inherited genetic diseases. Example 1; SEQ ID NO 21; 30pp; English.

The invention relates to a nucleic acid hybridisation probe comprising a labelled, single copy nucleic acids of at least 50 nucleotides, which will hybridise to a deduced single copy sequence interval in target uncleic acid (TNA) of known sequence. The single copy sequence is deduced by comparing the target sequence. The single copy sequence is deduced by comparing the target sequence. The probe is essentially free collection of high and low complexity repeat sequences as found in the collection of high and low complexity repeat sequences as found in the collection of high and low containing the target nucleic acid. The probe is genome of the organism from containing the target nucleic acid. The probe is generated by PCR on the target sequence. The probe is essentially free cof blocking nucleic acid sequences which will hybridise to repeat cof blocking nucleic acid sequences which will hybridise to repeat collecting a useful in a hybridisation method, where the hybridisation method is from in situ hybridisation method, where the hybridisation method is from in situ hybridisation, Southern blot, and cother methods in which nucleic acid which will confident and aduption or triplicon sequence domain. The probe is useful hybridises to the genome at more than three preferably ten different corputions as a determination of new repeat sequence from a cottermining achromeome breakpoint and is useful in the fields for determining a chromeosome breakpoint and is useful in the fields for cytogenetics may be used to enalyse specific chromosomal locations by in sight whore probes may be used to analyse specific chromosomal locations by in situ hybridisation as a detection of acquired or inherited genetic.

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diseases especially for detection of genetic or neoplastic disorders. Unlike prior art techniques, the probe permits more precise chromosomal breakpoint determinations by in situ hybridisation. The genomic sequence comprising the human HIRA gene (histone cell cycle regulation defective, S. cerevisiae, homologue A) was analysed for single copy sequence therevals for use as probes of the invention. HIRA is located on chromosome 22 as a duplicate, deletions of 1 copy lead to bideorge and velo-Cardio-facial syndromes. The present sequence is a high complexity repeat found within the human genome used to analyse the HIRA gene for repeat regions. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
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Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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                                                                                                            The present invention relates to new nucleic acid sequences of human endogenouse retrovirus, HERV-7q, which is located on chromosome 7q. Regulatory elements associated with HERV-7q may alter expression of other genes (even remote genes) on the same chromosome, inducing immunological and/or neurological changes (which may be pathological or protective/curative). HERV-7q peptides can be used to improve efficiency of the immunotesaponse, e.g. in immunotherapy. HERV-7q peptides and their coding sequences can be used in immunogenic or vaccinating compositions, for protection against autoimmune diseases, particularly multiple sclerosis. The peptides may also be used (by sequence comparison) to detect/identify endogenous retroviruses that are abnormally expressed in cancer, neuropathologies or other autoimmune diseases. The present sequence was used to illustrate the invention
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                                         nucleic acid sequences of human endogenous retrovirus, HERV-7q, used diagnosis, treatment and prevention of autoimmune and neurological
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                   WPI; 2000-160587/14
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The present invention describes a method (MI) for screening for an antineoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result
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of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oseophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous call carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
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The present sequence encodes a human endogenous retrovirus envelope protein. The specification describes a method for detecting expression of an envelope protein from a human endogenous retrovirus (HRRW), in cells, of a tissue or culture. The method comprises detecting syncytia formation polypeptides and polymorleotides for the envelope protein. Envelope prophylactic compositions, particularly for treatment of cancer, to correct defects in placental development (or other natural formation of other types of syncytia), and to promote adhesion of cells in grafts or cellular repair processes. Expression of sequences antisense to the polymucleotide are used to prevent formation of syncytia
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                                                                                                 Detecting expression of human endogenous retrovirus envelope protein cells of a tissue or culture, from its ability to induce syncytia.
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                                      CTTCCTTTTGTTATAGGAGCAGGGGTGCTAGGTGCTAGGTACTGGCATTGGCGGTATC
                                                                                                                                                                                             ACAACCTCTACTCAGTTCTACTACAAACTATCTCAAGAACTAAATGGGGACATGGAACGG
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                ACTGAACAAGATTTATACAATCATGTCGTACCTAAGCCCCCACAAAAGAGTACCCATT
                                                                                    CTICCTITIGITATCAGAGCAGGAGTGCTAGGCAGACTAGGTACTGGCATTGGCAGTATC
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syncytia; cancer; cell adhesion; ss.
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'product= "envelope protein"
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(INRM ) INST ŅAT SANTE & RECH MEDICALE
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15-SEP-1999;
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AAF55630
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New nucleic acid from human endogenous retrovirus, useful e.g. for diagnosis of autoimmune disease and complications of pregnancy, contains at least part of the gag gene.
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/note= "ORF2 52 AA" 7112. .7255 /*tag= f /note= "ORF3 48 AA" 7244. .7254

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                                        The present sequence represents an endogenetic retrovirus, which is associated with an autoimmune disease, and is integrated into the human genome. The retrovirus is human endogenous retrovirus (HERV-W). The HERV-W retrovirus is associated with autoimmune disease, failure of pregnancy or disorders of pregnancy. HERV-W nucleic acid fragments, or proteins derived from it, are useful for diagnosis of autoimmune disease (specifically multiple sclerosis) and for monitoring pregnancy. The nucleic acid fragments may also be used for in situ labelling of isolated chromosomes, while the transcription product can be used to study or monitor T cell proliferation in vitro
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Pred. No. 0;
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Disclosure; Page 49-52; 53pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                            89.4%;
92.2%;
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Best Local Similarity 92.2
Matches 1365; Conservative
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Autoimmune disease; retrovirus; human endogenous retrovirus W; HERV-W; gag gene; pregnancy; multiple sclerosis; T cell proliferation; ss.

Location/Qualifiers

Human endogenous retrovirus

Human endogenous retrovirus W (HERV-W) sequence.

(first entry)

07-NOV-2000

ВР

standard; DNA; 7582

AAA59215

RESULT 19

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This sequence represents the complete sequence of the human endogenous retrovirus (HERV) W genome. The nucleic acids, their fragments or peptides encoded by them are markers of autoimmune disease (e.g. multiple sclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulin- dependent diabetes and related pathologies) and of abnormal or unsuccessful pregnancy and can be used as chromosomal markers for susceptibility to these conditions, or proximity markers of genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid sequences from human endogenous retrovirus-W - expressed exclusively in placenta and useful in diagnosis and therapy of autoimmune disease, and abnormal or failed pregnancy.
                                                                                                                                                                                                                                                                                                 Clone; human endogenous retrovirus; genome; autoimmune disease; multiple sclerosis; rheumatoid polyarthritis; insulin-dependent diabetes; disseminated lupus erythematosus; pregnancy; chromosomal marker; ss.
                                                                                                      CTCAGCCAATGGATGCCCTGGGTTCTCCCTTTAGGACCTCTAGCAGCTCTAATATTG
                                                            TTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATT
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New human retrovirus HERV-W ENV proteins/peptides having superantigen activity useful for diagnosing and treating multiple sclerosis.

Claim 13; Fig 9; 94pp; English

Con the basis of the PBS t-RNA motif used for the classification of human endogenous retrovirus (HERVS) the full length endogenous provirus which endogenous retrovirus (HERVS) the full length endogenous provirus which endogenous retrovirus (HERVS) the full length endogenous proteins which designated HERVW. The present invention describes proteins or peptides (I) having superantigen (SAg) activity comprising the ENV protein (ENV) of HERVW, the surface protein (SU) and transmembrane (TM) sub-units. (I) have neuroprotective activity, and can be used in: vaccines; antisensetherapy; and HERV-W SAg activity-inhibitors. (I) and encoding DNA/RNA are useful for diagnoshing multiple sclerosis (MS) or HERV-W associated disorders. (I) are also useful for identifying substances (and optionally recovering) capable of binding to a retroviral superantigen associated with MS, substances capable of blocking SAg activity and substances capable of blocking transcription or translation of HERV-W retroviral superantigen associated derived from (I), modified to be devoid of SAg activity and being capable of generating an immune response against HERV-W retroviral sag is useful in therapy. Nucleic acid capable of blocking SAg activity, capable of blocking transcription or translation of HERV-W retroviral saginated for use in treatment and preventing MS. obtained using (I) are useful for the treatment and preventing of preventing of MS. (I) and nucleic acide encoding them are useful for diagnosing autoimmune disease. The present sequence encodes the geocifically claimed envelope protein of HERV-W designated G encoding them are useful for specifically claimed envelope protein of HERV-W designated G

Sequence 2782 BP; 741 A; 768 C; 564 G; 709 T; 0 U; 0 Other;

1242 1002 1062 1122 ö 240 300 360 420 120 180 942 822 882 9 823 GCACCCCCCCCATGCCGCTGTATGACCAGTAGCTCCCCTCACCCAGAGTTTCTATGGAGA Arecaecerceegaaararreareceeareeraraeaacrerrreraageaaceee ACCTICACTGCCCACACCATATGCCCCGCAACTGCTATAACTCTGCCACTCTTTGCATG Accricacitécceacacecatarécecedaaciéciareacitécécecatrifécaré GGAGTCACTGTTGGTTGGACTTACTTCACCCAAACTGGTATGTCTGATGGGGGGTGGAGTT caagarcaggcaagagaaaaacargraaagaagraarcrcccaacrcacggggracar AGCACCCCTAGCCCCTACAAAGGACTAGTTCTCTCAAAACTACATGAAACCTCCGTACC GCACCCCCTCCATGCTGTACAACCAGTAGCTCCCCTTACCAAGAGTTTCTATGAAGA ACGCGGCTTCCTGGAAATATTGATGCCCCCATCATATAGGAGTTTATCTAAGGGAAACTCC CATGCAAATACTCATTATTGGACAGGAAAATGATTAATCCTAGTTGTCCTGGAGGACTT GGAGCCACTGTCGTTGGACTTACTTCACCCATACCAGTATGTCTGATGGGGGTGGAATT CAAGGTCAGGCAAGAAAAAAAAGTAAAGGAAGCAATCTCCCAACTGACCCGGGGACAT ATGGCCCTCCCTTATCATACTTTTCTCTTTACTGTTCTCTTACCCCCTTTCGCTCTCACT Gaps DB 5; Length 2782; ö Indels 108; 88.3%; Score 1308.2; 92.7%; Pred. No. 0; iive 0; Mismatches Best Local Similarity 92.7 Matches 1373, Conservative 943 1003 1063 Н 1123 121 883 181 361 421 61 241 301 Query Match 셤 셤 ठ g g ઠે 유 g ò ò ઠે 원 ò ò ઠે

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RESULT 22 AAX25661

AAX25661 standard; cDNA to mRNA; 2782

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid sequences from human endogenous retrovirus-W - expressed exclusively in placenta and useful in diagnosis and therapy of autoimmune disease, and abnormal or failed pregnancy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents clone cl.PH74 of the human endogenous retrovirus (HERV) W genome. The nucleic acids, their fragments or peptides encoded by them are markers of autoimmune disease (e.g. multiple sclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulintenancial dispetes and related pathologies) and of abnormal or unsuccessful pregnancy and can be used as chromosomal markers for susceptibility to these conditions, or proximity markers for
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                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid from human endogenous retrovirus, useful e.g. for diagnosis of autoimmune disease and complications of pregnancy, contains at least part of the gag gene.
                                                                                                                                                                                  HERV-W;
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                                                                                                                                                     gene, and 3' non coding sequences of HERV-W
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                                                                                                                                                                              Autoimmune disease; retrovirus; human endogenous retrovirus W; gag gene; pregnancy; multiple sclerosis; T cell proliferation;
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      GAAGCTGTGAAACTACAAATGGAGCCCAAGATGCAGTCCAA 2243
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Pred. No. 0;
0; Mismatches
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92.6%;
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Matches 1372; Conser
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                               CTCAGCCGATGGATGCCCTGGATTCTCCCCTTTAGGACCTCTAGCAGCTATAATATTG 2142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present DNA sequence was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang J;
Wang Z;
                    TTACTCCTCTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATT
                                                                                                                                                                                                                    novel gene; novel protein; tissue marker; molecular weight marker;
chromosome marker; genetic disorder; contig; ds.
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ou P, Drmanac RT,
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                                                              GAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAACCCCA 1481
                                                                           2203 GAAGCTGTGAAAACTACAAATGGAGCCCAAGATGCAGTCCAA 2243
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    Ren F, Zhang
Weng G, Zhou P,
Boyle BJ;

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llarity 93.0%; Pred. No. 0;
Conservative 0; Mismatches
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                                                                                                                                                                                                    nucleotide
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                                                                                                                                       BP.
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11-DEC-2001; 2001US-0339453P.

14-MAR-2002; 2002US-036591P.

14-MAR-2002; 2002US-0365384P.

12-APR-2002; 2002US-0372381P.

12-APR-2002; 2002US-037261SP.

22-APR-2002; 2002US-0012858.

24-APR-2002; 2002US-0376045P.
                                                                                                                                      ADE09587 standard; DNA; 3464
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                                                                                                                                                                               entry)
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Matches 1383; Conserv
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1610 ACCTTCACTGCCCACCACATATGCCCCGCAACTGCTATCACTCTGCCACTCTTTGCATG
                                                                                                                                                                                                                                              CAAAACCCCTACTAACTGTTGGATGTGCCTCCCCTGCACTTCAGGCCATACATTCAATC
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                                                            181 ACCTTCACTGCCCACACCCCATATGCCCCGCAACTGCTATAACTCTGCCACTCTTTGCATG
                                                                                                                                                          CATGCAAATACTCATTATTGGACAGGGAAAATGATTAATCCTAGTTGTCCTGGAGGACTT
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                                         <u>ACGCGGCTTCCTGGAAATATTGATGCCCCATCATATAGGAGTTTATCTAAGGGAAAACTCC</u>
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(I). The polynucleotides (I) can be used as hybridisation probes, oligomers or primers, for chromosome or gene mapping, for the recombinant production of proteins, and for generating antisense DNA or RNA. The present sequence represents a human contig polynucleotide sequence, which is used in an example from the present invention.
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                                                                                                                                                                                Length 9502;
                                                                                                                                        Sequence 9502 BP; 2813 A; 2433 C; 1992 G; 2263 T; 0 U; 1 Other;
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                                                                                                                                                                                                                               98;
                                                                                                                                                                                  Score 1298.2;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                       87.7%;
93.0%;
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Best Local Similarity 93.0
Matches 1383; Conservative
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primer; chromosome mapping; gene mapping; recombinant protein production;
human; gene; 88.
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                                     GTCCTTCAAAATCGAAGAGCTTTAGACTTGCTAACCGCTGAAAGAGGGGGAACCTGTTTA
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                                                                                                                      New nucleic acid sequences of human endogenous retrovirus, HERV-7q, us-
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disease; HERV-7q; chromosome 7q; immunotherapy; plerosis; ds.

Human endogenous retrovirus

29-DEC-1999

multiple sclerosis;

Autoimmune

BP.

ABN97931 standard; DNA; 1799

RESULT 27 ABN97931/c

(first entry)

01-AUG-2002

ABN97931

retroviral

Human

1403

360

1463

300

1643

120

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Gaps

32;

87; Indels

Length 1799;

DB 3;

Score 1278.8; Pred. No. 0; 0; Mismatches

1 AIGGCCCICCCITAICAIACII

1703

1523

1583 240

ACGCGGCTTCCTGGAAATATTGATGCCCCATCATATAGGAGTTTATCTAAGGGAAACTCC ACCTTCACTGCCCACACCCATATGCCCCGCAACTGCTATAACTCTGCCACTCTTTGCATG

1642

181

121

GCACCCCTCCATGCTGCTGTACAACCAGTAGCTCCCCTTACCAAGAGTTTCTATGAAGA

61

1343

420

1223

540

900

1283

Cytostatic; carcinoma; lymphoma; cancer; human; gene;

WO2003073826-A2.

12-SEP-2003

Homo sapiens

genomic sequence hCG32959

Human

(first entry)

18-NOV-2004

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ACN44334 standard; DNA; 161334 BP

ACN44334/C RESULT 28

ACN44334

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                are associated with Carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of bioactive agent capable of bioactive agent capable of bioactive agent capable of modulating the activity of CAP; (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating carcinoma; (vii) for neutralizing the effect of CAP; (vii) for treating (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number in addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent US2002182586A1, for which no sequence data was published
                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention relates to novel DNA and protein sequences which
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92.5%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 730; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleotide sequence.
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                                                                                                                                                                                                                                                                    01-MAR-2002; 2002US-00087192
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Best Local Similarity
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Regulatory elements associated with HERV-7q may alter expression of other genes (even remote genes) on the same chromosome, inducing immunological and/or neurological changes (which may be pathological or protective/curative). HERV-7q peptides can be used to improve efficiency of the immune response, e.g. in immunotherapy. HERV-7q peptides and their coding sequences can be used in immunogenic or vaccinating compositions, for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protection against autoimmune diseases, particularly multiple sclerosis. The peptides may also be used (by sequence comparison) to detect/identify endogenous retroviruses that are abnormally expressed in cancer, neuropathologies or other autoimmune diseases. The present sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid sequences of human endogenous retrovirus, HERV-7q, use
for diagnosis, treatment and prevention of autoimmune and neurological
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                                                                                                                                                                                                                                                                                                                                                                                    HERV-7g; chromosome 7g; immunotherapy,
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nilarity 91.0%;
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The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of expression, the probes are therefore useful in grading and/or staging of flaseases of the cervix. Intably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fig. wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene expression analysis in human cervical cell sample.
                              2147 ACCGAGAAAGTTAAAGAAATTCAAGGTCGAATATAACGTAGAGCAAAGGAGCTGGAAAAC
                                                                                                   CTAGCAGCTCTAATATTGTTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAG
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           ACTGAGAAAGTTAAAGAAATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAAAAC
                                                                                ACCGAACGCTGGGGCCTCCTCAGCCAATGGATGCCCTGGGTTCTCCCCTTCTTAGGACCT
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Pred. No. 0;
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26-MX-2000; 2000US-0207456P.
30-UJN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-023468IP.
27-SEP-2000; 2000US-023468IP.
04-OCT-2000; 2000GB-00024263.
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30-UJN-2000; 2000US-00608408.
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived nucleic acid probes for measuring gene expression in a sample derived crow human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probes size useful for verifying the carbession of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this partent did not form part of the princed specification, but was obtained in electronic format directly from WIPO at the princes.
                                 New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
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21-SEP-2000; 2000US-0234687P.
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30-JUN-2000; 2000US-00608408.
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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Sequence 1894 BP; 557 A; 500 C; 361 G; 476 T; 0 U; 0 Other;
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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver. comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABSS5011-ABSS1005 represent human liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed appecification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                    1423
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                                                                                                                                                                                                                                                                                                                                     TTGTCTTCCAGAATTGAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAACCCCA 1481
                                                                                                                                                                                                                                                                                                                                                                            CCGAGAAAGTTAAAGAAATTCAAGGTCGAATATAACGTAGAGCAAAGGAGCTGCAAAACA
                                                                                                     CTGGACCCTGGGGCCTCCTCAGCCAATGGATGCCCTGGATTCTCCCCTTCTTAGGACCTC
                                                                      CCGAACGCTGGGGCCTCCTCAGCCAATGGATGCCCTGGGTTCTCCCCCTTCTTAGGACCTC
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hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
coronary heart disease; ss.
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
21-SEP-2000; 2000US-0053366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
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	RESULT 38 AA104422 ID AA104422 ID AA104422 XX AC AA104422; XX DT 09-OCT-2001 (first entry) XX DT Nobe #4413 used to measure gene expression in human breast sample. XX XX DT Nobe; human; breast disease; breast cancer; development disorder; ss; XX XX XX XX XX YX YX YX YX YX YX YX YX	XX XX 04-FEB-2000; 2000US-0180312P. PR 26-MAY-2000; 2000US-0180312P. PR 30-JUN-2000; 2000US-0207456P. PR 30-JUN-2000; 2000US-00662366. PR 30-JUN-2000; 2000US-023468P. PR 27-SEP-2000; 2000US-023468P. PR 27-SEP-2000; 2000US-023468P. PR 27-SEP-2000; 2000US-023468P. PR 27-SEP-2000; 2000US-023468P. RX (MOLE-) MOLECULAR DYNAMICS INC. XX XX XX WHI; 2001-476286/51.	Novel single exon nucleic acid probe used to measuring gene expression in PT a human breast. XX Claim 25, SEQ ID NO 4413; 322pp; English. XX CThe present invention relates to novel single exon nucleic acid probes. CThe present equence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe CC whorldises at high stringency to a nucleic acid expressed in the human cc probes are useful for predicting, diagnosing, grading, contioning and prognosing diseases of the human breast. CC breast. The probes are useful for predicting, diagnosing, grading, contioning and prognosing diseases of the human breast. CC particularly those diseases with polygenic actiology. The diseases include: breast diseases with polygenic actiology. The diseases of the breast, fibrocystic changes, proliferative breast disease and nonce arctinoma tumours. Note: The sequence data for this patent did not form carcinoma tumours. Note: The sequence data for this patent did not form the printed specification, but was obtained in electronic format XX XX XX XX XX XX XX XX XX XX
Query Match 76.4%; Score 1131.6; DB 4; Length 1894; Best Local Similarity 92.4%; Pred. No. 0; Mismatches 84; Indels 16; Gaps 2; Matches 1218; Conservative 0; Mismatches 84; Indels 16; Gaps 2; QY 164 TATCTAAGGGAACTCCACCTTCACTGCCCACACCCATATGCCCCACACTGCTATAACT 223 Db 1 TATCTAAGGGAACCCCCACCTTCACTGCCACCCCATATGCTCAACTTAATTGACTAAACT 60 Oy 224 CTGCCACTCTTTGCATGCAAGAATACTCATTATTGGACAGGAAAACGATTAATCCCA 120 Db 61 CTGCCACTCTTGCATGCAATACTCATTATTGGACAGGAAAACGATTATTCCA 120 QY 284 GTTGTCCTGGAGGACTTGGAGCACTCTTTTATTGGACTACTCATCATTATTCCA 120 Db 121 GTTGTCTGGAGGACTTGGAGCACTCTTTTATTGGACTATAATCTTCACCATTATTTTTTTATTCATTC	404 AACTGACCCGGGGACATAGCACCCCTACAAAGGACTAGTTCTCTCAAAACTAC 463	TCACCTGTGTAAAATTTAGCAATACTATAGACACACACGGCTCCCAATGCTCGTCGTGTGTAAAATTTAGCAATACTATAGACACACAC	705 CCCCTATGCCCATCTACACTGAACAAGATTATACAATCATGTCATACCTGAGCCCGGG 764 944 ACAAAAGACTACCCATTCTTCTTTTTTACAGAGCAGAGTGCTAGGCAGACTAGGTA 1003 765 ACAAAAGACTACCCATTCTTCCTTTTGTTATTGAGCAGAGTGCTAGGCAGACTAGCTA 824 1004 CTGGCATTGGCAGTACCACACCTCTACTCAGTTCTACACAAACTACTCAGAAATAA 1063 825 CTGGCATTGGCAGTATCACAACCTCTACTCAGTTCTACAAACTTCTCAAGAAATAA 1063 1064 ATGGTGACATGGCAGTACCACACCTCTACTCAGTTCTTACAACTTCACAAAAAAAA

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                                                                                                                                                                                                                                                                                                                                                                                                 Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histicoytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dyskinesis; pulmonary hypertension; hypertension; hyaline membrane disease.
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26-MAY-2000; 2000US-0207456P.
30-UNA-2000; 2000US-0608408.
03-AUG-2000; 2000US-0053366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
04-OCT-2000; 2000GB-00024263.
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                      76.4%; Score 1131.6;
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complements or the 12387 open reading frames derived from the 12614

probes. Also included are a microarray comprising the novel set of probes

if the novel set of probes which hybridise at high stringency to a nucleic

acid expressed in the human lung; measuring gene expression in a sample

collection of detectably labeled nucleic acids derived from human lung

collection of detectably labeled nucleic acids derived from human lung

collection of detectably bound to each probe of the

algorithmically predicting at least one exon from genomic sequences of

the eukaryote; and (b) detecting specific hybridisation of detectably

clabeled nucleic acids from eukaryote; genome, comprising (a)

algorithmically predicting at least one exon from genomic sequences of

the eukaryote; and (b) detecting specific hybridisation of detectably

comprising (a) identifying axons from genomic sequences of

the above mentioned microarray; assigning exons to a single gene,

comprising (a) identifying axons from genomic sequence by the method

above and (b) measuring the expression of each of the exons in several

conversation of the exons in the tissues and/or cell types uning hybridisation to a single exon

microarrays having a probe with the exon, where a common pattern of

expression of the exons in the tissues and/or cell types indicates that

confidence in the exons should be assigned to a single gene; a peptide comprising one

confidence in the exons in the tissues and/or cell types indicates that

confidence in the exons should be assigned to a single gene; a peptide comprising one

confidence, chronic obstructive pulmonary disease (COPD), interstitial lung

disease (LID), familial ideopathic pulmonary disease such as asthma, lung

cancer, chronic obstructive pulmonary disease such as asthma, lung

disease (LID), familial ideopathic pulmonary disease, pulmonary dystease, pulmonary hypertension and hyaline membrane disease. The

Cherous sclerosis, daucher's disease, with enempredicated propersory a general sequence is a single ftp.wipo.int/pub/published_pct_sequences \$\$GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG

Sequence 1894 BP; 557 A; 500 C; 361 G; 476 T; 0 U; 0 Other;

120 227 643 467 223 283 343 167 403 463 523 407 228 AACTGACCTGGGTACATAGCACCCCTGGCCCCTACAAAGGACTAGATCTCTCAAAACTAC 287 288 ATGAAACCTCCATACCCATACTGGCTGGTAAGCCTATTTAATACCACCTGACTGGGC 347 TCCATGAGGTCTCAGCCCAAAACCCTACTAACTGTTGGATGTGCCTCCCCCTGCACTTCA 583 9 CTGCCACTCTTTGCATGCATGCAATACTCATTATTGGACAGGAAAAACGATTAATCCCA CTGATGGGGGTGGAGTTCAAGATCAGGCAACAGAAAAACACATAAAGGAAGTAATCTCCC TCCATGAGGTCTCGGCCCAAAACCCTACTAACTGTTGGATGTGCCTCCCCCTGCACTTTA GGCCATACATTTCAATCCCTGTTCCTGAACAATGGAACAACTTCAGCACAGAAATAAAACA GGCCATACATTTCAATCCCTATACCTGAACAATGGAACAACTTCAGCACAGAAATAAACA 164 TATCTAAGGGAAACTCCACCTTCACTGCCCACACCCCATATGCCCCGCAACTGCTATAACT TATCTAAGGGAACCCCCACCTTCACTGCCCACATATGCCCCACAAACT CTGCCACTCTTTGCATGCATGCAAATACTCATTATTGGACAGGGAAAATGATTAATCCTA CTGATGGGGGTGGAATTCAAGGTCAGGCAAGAGAAAAACAAGTAAAGGAAGCAATCTCCC AACTGACCCGGGGACATAGCACCCCTAGCCCCTACAAAGGACTACTCTCTCAAAACTAC ATGAAACCCTCCGTACCCATACTCGCCTGGTGAGCCTATTTAATACCACCCTCACTCGGC Gaps Query Match 76.4%; Score 1131.6; DB 6; Length 1894; Best Local Similarity 92.4%; Pred. No. 0; Matches 1218; Conservative 0; Mismatches 84; Indels 16; 168 224 121 344 524 61 284 404 464 584 108 ď ద 셤 ઠે 셤 ठ 셤 δ δ ઠે a ઠે g ઠે

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TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHY
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ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPETATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,847B
FILING DATE: 26-No. 6582703-1997
CLASSIFTATION: AUNKNOWN:
ATTORNEY/AGENT INFORMATION:
NAME: BERIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELEPAX: 703-836-6400
TELEPAX: 703-836-6400

TELEPAX: 703-836-6400

TELEPAX: 703-836-2787

INPORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 1481 base pairs

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KOMURIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
MANDRAND, BENARD
GARSON, JEREMY
TUKE, PHILIP
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STREET: P.O. BOX 19928
CITY: ALEXANDRIA
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BESEME, FREDERIC
BEDIN, FREDERIC
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CORRESPONDENCE ADDRESS
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GENERATI Sequence 21, Application US/09573080A
Sequence 21, Application US/09573080A
Sequence 21, Application US/09573080A
GENERAL INFORMATION:
APPLICANT: NOGAN: WOLL
APPLICANT: ROGAN: PETER
TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF (FILE PEFERENCE: 30307
CURRENT APPLICATION UNMBER: US/09/573,080A
CURRENT FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 479
SOFTWARE: Patentin version 3.0
SEQ ID NO 21
LENGTH: 8523 7328 7028 7088 7148 7268 6968 ö 420 240 300 360 120 180 CAAGATCAGGCAAGAGAAAAACATGTAAAAGAAGTAATCTCCCAACTCACCGGGGTACAT CATGCAAATACTCATTATTGGACAGGGAAAATGATTAATCCTAGTTGTCCTGGAGGACTT <u> Arecaecercecesaaararrearececearecraraesaererrreraaesaacecec</u> GGAGCCACTGTCTGGACTTACTTCACCCATACCAGTATGTCTGATGGGGGTGGAATT ACCTICACTGCCCACACCATAIGCCCCCCACACTGCTATAACTCTGCCACTCTTTGCATG 361 CAAGGTCAGGCAAGAAAAACAAGTAAAGGAAGCAATCTCCCAACTGACCGGGGACAT GCACCCCTCCATGCTGCTGTACAACCAGTAGCTCCCCTTACCAAGAGTTTCTATGAAGA 121 ACGCGGCTTCCTGGAAATATTGATGCCCCATCATATAGGAGTTTATCTAAGGGAAACTCC Gaps) DATE: 1992-10-) DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase)) DATABASE ENTRY DATE: 1996-01-26 1 DATABASE ENTRY DATE: 1996-01-26 ô Length 8523; 1 ATGGCCCTCCCTTATCATACTTTTCTCTTTACTGTTCTCTTTACCCCCT Indels FEATURE:
NAME/KEY: repeat_region
LOCATION: (1)..(8523)
OTHER INFORMATION: herv17
PUBLICATION INFORMATION:
AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A
TITLE: Protchypic sequences for human repetitive DNA
JOURNAL: Journal of Molecular Evolution DB 4; 92; 90.1%; Score 1333.8; ilarity 93.8%; Pred. No. 0; Conservative 0; Mismatches TYPE: DNA ORGANISM: Homo sapiens Similarity ISSUE: 4 PAGES: 286-291 Query Match Best Local Simil Matches 1389; C 7209 6849 181 241 301 61 6969 임 셤 ò 셤 8 셤 ò 셤 ò g à 셤 ઠ ઠ ò

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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PAPLICATION NUMBER: 60/231,498

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 17382
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Matches 1389; Conser
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                                        CAAAACCTACTAACTGTTGGATGTGCCTCCCCTGCACTCAGGCCATACATTTCAATC
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RESULT 5 US-09-949-016-17382 Sequence 17382, Application US/09949016 ; Patent No. 6812339

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Pred. No. 0;
0; Mismatches
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Best Local Similarity 92.5%;
Matches 1399; Conservative
; LENGTH: 145320
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15858
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF ILLUS DATE: 2000-04-14
CURRENT FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRAEESEQ FOR WINGOWS VERSION 4.0
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US-09-949-016-15858/c
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Pred. No. 2.4e-87;
0; Mismatches 25; Indels
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                                ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
6582703-1997
                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA SEQUENCE DESCRIPTION: SEQ ID NO: 108:
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MCOY, John
APPLICANT: LaVallie, Edward
APPLICANT: Racie, Lisa
APPLICANT: Racie, Lisa
APPLICANT: Reacie, Lisa
APPLICANT: Preacy, Maurice
APPLICANT: Evans, Cheryl
APPLICANT: Evans, Cheryl
TITLE OF INVENTION: SECRETED PROTEIN
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSE: Genetic
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FILING DATE: 26-No. 65827
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                          LENGTH: 1329 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 108:
                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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Best Local Similarity 92.7%;
Matches 317; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: Massachusetts
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ASSOCIATED WITH MULITPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
THERAPEUTIC PURPOSES
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
OPERATING SYSTEM: PC-DOS/NS-DOS
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BESENE, FREDERIC
BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOWURIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
MANDRAND, BERNARD
GARSON, JEREM
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CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
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                                                                                                                                                                                                                                                                                                                                              1200 AGGAGAAGAACGCTG------
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Indels
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Pred. No. 7.7e-46;
0; Mismatches 17;
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                 ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 848-824
TELEPAX: (617) 846-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 542 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                              11.7%;
ilarity 91.5%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.2%
Matches 320; Conservative
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US-08-721-489-2
                                                                                                                                                                                                                            linear
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     CLASSIFICATION:
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; ORGANISM: Human
US-09-949-016-184496
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Matches 184;
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JOS-01-711-89-7.

JOS-01-711-89-7.

JOSERRAL INFORMATION:

APPLICANT: Jacobs, Kenneth
APPLICANT: Lavallie, Edward
APPLICANT: Lavallie, Edward
APPLICANT: Merberg, David
APPLICANT: Spaulding, Vikki
JITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 cambridge
CITY: Cambridge
STATE: Massachusetts
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: PRODES: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
APPLICATION NUMBER: US/08/721,489
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                               Length 542;
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
SUGTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/686,878A
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELEPHONE: (617) 848-824
TELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTER(STICS:
LENGTH: 542 base pairs
TYPE: nucleic acid
TYPE: MANNEDDESS: double
                                                                                                                                                                                                                                                                                                                                                                                                             Score 173.8; DB 1;
Pred. No. 7.7e-46;
0; Mismatches 17;
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Best Local Similarity 91.5%;
Matches 184; Conservative (
                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: cDNA
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RESULT 10

US-09-99-016-184496/c

j Gequence 184496, Application US/09949016

j Patent No. 6812339

j GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

PRICE REFERENCE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PELING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 184496
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Length 542;
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Sequence 17026, Application US/09949016
; Sequence 17026, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TILE REFERENCE: CL001307
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID MOS: 2070102
; SOFTWARE: FRASESQ for Windows Version 4.0
; TENGTH: 1000700
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59.8%; Pred. No. 5.2e-40;
tive 0; Mismatches 212;
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17026
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ORGANISM: Human
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Best Local S:
Matches 324
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                             GGTAATCCAACCAACTGCTGGATGTGTCTCCCCTTGCA-TTTTCAATGTATGTCCCAGTC
                                                                                                                                                                                      CCTGTTCCTGAACAATGGAACAACTTCAGCACAGAAATAAACACCACTTCCGTTTTAGTA
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                                                     CAAAACCCTACTAACTGTTGGATGTGCCTCCCCTGCACTTCAGGCCATACATTCAATC
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59.8%; Pred. No. 5.2e-40;
iive 0; Mismatches 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12707, Application US/09949016 Patent No. 6812339
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US-09-949-016-12707
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Matches 324; Conservative
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LENGTH: 190078
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Sequence 20251, Application US/09949016;
Sequence 20251, Application US/09949016;
Batent No. 681239
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOOL307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 2007012
SOFTHARE: PRESEEQ for Windows Version 4.0
SEQ ID NO 202251
LENGTH: 601
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US-09-949-016-17417/C

JSGQUENCE 17417, Application US/09949016

REGION OF 681239

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR PLILING DATE: 2000-10-03
PRIOR PLILING DATE: 2000-10-03
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PRIOR PLILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PLILING DATE: 2000-10-08
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Pred. No. 2.5e-38;
0; Mismatches 32
183 CTTCACTGCCCACACCCATATGCCCCGCAACTGC 216
                                                                     477 TTTCACCATCCACACCCATATGCCCCTGCACTTC 510
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ilarity 84.6%;
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US-09-949-016-202251
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US-09-949-016-202251
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Matches 181;
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; Sequence 202256, Application US/09949016

; Fatent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VEWTER, 
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Pred. No. 2.5e-38;
0; Mismatches 32;
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Best Local Similarity 84.6%;
Matches 181; Conservative C
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; ORGANISM: Human
US-09-949-016-202250
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3: Oliff & Berridge
700 South Washington Street, Suite 300
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                           16027 TTCACCATCCACACCCATATGCCCCTGCACTTC
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REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                     Sequence 58, Application US/08691563C Patent No. 6001987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION TELEPHONE: 703-836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 55.7%;
Matches 302; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1722 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1722 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleotide
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Herve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
STREET: 70
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SEQUENCE 12249, Application US/09949016

PATENT NO. 6812339

PRICENT NO. 6812339

TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PELICATION NUMBER: 60/241,755

PRIOR PELICATION NUMBER: 60/241,755

PRIOR PELICATION NUMBER: 60/241,768

PRIOR PELICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREESEQ for Windows Version 4.0
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Pred. No. 5.3e-37;
0; Mismatches 32;
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                                                                                                                                             Score 150.8; DB Pred. No. 5.3e-37 0; Mismatches 3:
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OTHER INFORMATION: n = A,T,C or G
                                                           10.2%;
84.6%;
                                                                                                                                           Query Match
Best Local Similarity 84:68;
Matches 181; Conservative
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Best Local Similarity 84.6
Matches 181; Conservative
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NAME/KEY: misc_feature
                       FEATURE:
NAME/KEY: misc_feature
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LENGTH: 77997
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APPLICANT: Frederic BESEME
APPLICANT: Frederic BESEME
APPLICANT: Frederic BEDIN
APPLICANT: Frederic BEDIN
APPLICANT: Glaucia PARANHOS-BACCALA
APPLICANT: Colette JOLINEA
APPLICANT: Colette JOLINEA
APPLICANT: Colette JOLINEA
APPLICANT: COLETTE JOLINEA
APPLICANT: BEINAR MANDRAND
TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
TITLE OF INVENTION: THERAPEUTIC PURPOSES
CORRESPONDENCE: 92
CORRESPONDENCE: 92
CORRESPONDENCE: 92
CORRESPONDENCE ADDRESS:
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Pred. No. 2.4e-36;
0; Mismatches 234; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/691,563C FILING DATE: 02-AUG-1996
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GARSON, JEREMY
GARSON, JEREMY
TUKE, PHILIP
TUKE, PHILIP
TUKE, PHILIP
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYI
THERAPBUTIC PURPOSES
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                                                                                                                               346 CAGTGCAGAGCCATACAACTAATATCCCTATTTATAGGGTTAGGAATGGCTACTGCTACA
                                                                                                                                                                        1000 GGTACTGGCATTGGCAGTATCACAACCTCTACTACTACTACTACTACTATCTCAAGAA
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                                                                                             940 CACAACAAAAGAGTACCCATTCTTCTTTTGTTATCAGAGCAGGAGTGCTAGGCAGACTA
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                                                      9
                  Length 1722;
                                                      Indels
                Score 145.6; DB 4;
Pred. No. 2.4e-36;
0; Mismatches 234;
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ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 54, Application US/08979847B
Patent No. 6582703
GENERAL INFORMATION:
APPLICANT: PERRON, HERVE
BESEME, FREDERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BEDIN, FREDERIC
PARANHOS-BACCALA, G
KOMURIAN-PRADEL, FL
JOLIVET-REYNAUD, CO
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ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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GARSON, JEREMY
                    9.8%;
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                                                        Conservative
                                        Similarity
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                                        Best Local Sim
Matches 302;
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APPLICANT: Herve PERRON
APPLICANT: Frederic BESEME
APPLICANT: Frederic BESEME
APPLICANT: Frederic BEDIA
APPLICANT: Glaucia PARANHOS-BACCALA
APPLICANT: Gloucia PARANHOS-BACCALA
APPLICANT: Colette JOLIVET
APPLICANT: Colette JOLIVET
APPLICANT: Bernard MANDRAND
APPLICANT: BERNARHON: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
TITLE OF INVENTION: THERAPEUTIC PURPOSES
TITLE OF INVENTION: THERAPEUTIC PURPOSES
CORRESPONDENCE ADDRESS:
ADDRESSES: Oliff & Bernidge
ADDRESSES: Oliff & Bernidge
ADDRESSES: Oliff & Bernidge
                                                                                                                                                                                                                    1419
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                                                                                                                                       1359
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1300 AACACCGAACGCTGGGGCCTCCTCAGCCAATGGATGCCCTGGGTTCTCCCCCTTAGGA
                                                                                                                                                                                                                  1360 CCTCTAGCAGCTCTAATATTGTTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTT
                                                            1240 GTCACTGAGAAAGTTAAAGAAATTCGAGATCGAATACAATGTAGAGCAGGAGCTTCAA
                                                                                                 646 GTACGAGATGCCACCTGGCATTTACAGGAAAGGGCTTCTGATATCAGACAATGCCTTTCA
                                                                                                                                                                              706 AACTCTTATACCAA-----CCTCTGGAGTTGGGCAACATGGCTTCTTCCATTTCTAGGT
                                                                                                                                                                                                                                                                                                1420 AAGTTTGTCTTCCAGAATTGAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 700 South Washington Street, Suite 300 CITY: Alexandria STATE: Virginia CUNTRY: U.S.A. ZIP: 2214 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATING SYSTEM: PC-DOS/MS-DOS SOUTHARE: PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
RECISERNCE/DOCKET NUMBER: WPB 38588
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/691,563
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/374,766
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 58, Application US/09374766
Patent No. 6579526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 703-836-2787

INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 1722 base pairs
TYPE: nucleotide
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
US-09-374-766-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             1480 CA 1481
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SEQ ID NO 249
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCCTAGCAGCAGTAGTCCTTCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGA 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1240 GTCACTGAGAAAGTTAAAGAAATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAA 1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1300 AACACCGAACGCTGGGGCCTCCTCAGCCAATGGATGCCTTGGGTTCTCCCCTTTTAGGA 1359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1420 AAGTTTGTCTTCCAGAATTGAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAACCC 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1060 ATAAATGGTGACATGGAACAGGTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAAC 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      706 AACTCTTATACCAA-----CCTCTGGAGTTGGGCAACATGGCTTCTTCTAGGT 759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1360 CCTCTAGCAGCTCTAATATTGTTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    466 ricrcadacagrridodagaaaraargaaricraficriracrifadaarccaarragad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    586 GGAGGACTCTGCACCTTCTTAGGGAAGAGTGTTTTTTTTACACTAACCAGTCAGGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       346 CAGTGCAGAGCCATACAACTAATATCCCTATTTATAGGGTTAGGAATGGCTACTGCTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               646 GTACGAGATGCCACCTGGCATTTACAGGAAAGGGCTTCTGATATCAGACAATGCCTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     940 CACAACAAAAGAGTACCCATTCTTCCTTTTGTTATCAGAGCAGGAGTGCTAGGCAGACTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
COMPUTER: IBM PC compatible
COMPUTER: TBM PC.DOS/MS.DOS
COFFRARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RAPLICATION WHOBER: US/08/979,847B
FILING DATE: 26-No. 6582703-1997
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 2.4e-36;
0; Mismatches 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.8%; Score 145.6; Best Local Similarity 55.7%; Pred. No. 2.4 Matches 302; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                  TYPE: nucleotide

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: US-08-979-847B-54
                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1722 base pairs
                                                                                                                                                                                                                     TELEPHONE: 703-836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA 1481
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RESULT 20 10S-09-799-451-249 ; Sequence 249, Application US/09799451 ; Patent No. 6783969

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1379 TGTTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCGGAA 1438
1865 TTTTGCTCCTTTTTGGTCCATGTCTCCTAATCTAATAACCCAATTTGTCTCCTCTCGCC 1924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1319 TCCTCAGCCAATGGATGCCTGGGTTCTCCCCTTTAGGACCTCTAGCAGCTCTAATAT 1378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1505 caaaagciriccircacciaragccagciricaaagaaaaragaaaracaacaacaacaricacca 1564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1805 GAACTTGGAAAHGGTHCTCTHGGGHTCTTCCCCTHACAGGCCCACTTGTTAGTCTCCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2908;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.8%; Score 144.6; DB 4;
56.9%; Pred. No. 7.1e-36;
tive 0; Mismatches 214;
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6783969el Nucleic Acids
TITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pt_Fugenes Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTGAAGCTGTAAAGCTACAGATG 1461
                                                                                                                        Zhao, Qing A.
Wang, Jian-Rui
Ma, Yunqing
Yamazaki, Victoria
Chen, Rui-hong
Zhou, Ping
Goodrich, Ryle
Asundi, Vinod
Ren, Feiyan
                                                                                                                                                                                                                                                                Yonghong
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                                                                                      Zhang, Jie
Xue, Aidong J.
                                                                                                                                                                                                                              Wang, Zhiwei
                                                                                                                                                                                                                                                                                                                 Ghosh, Reena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (382) .. (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 286; Conserv
                                                                                                                                                                                                                                                                                            Wehrman,
                                                                                                                                                                                                                                                                           Yang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (382
US-09-799-451-249
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APPLICANT: INC.V. INC.V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1152 citactricialarcecalarasacterrissesses 1211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1096 GICACCTIGGAAGAICAACTITAACTCCCTAGCAGTAGTCCTTCAAAATCGAAGAGCT
1420 AAGTTTGTCTTTCCAGAATTGAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAACCC
                                    8142 AAATTGTTTCCTCTAGAATCAAGGCCATCAAGCTACAGATGGTCTTACAAATGGAACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691,563C
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET UNMBER: 39,024
REFERENCE/DOCKET UNMBER: WPB 38588
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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57.6%; Pred. No. 1.2e---.
6; Mismatches 183;
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                                                                                                                                                                                                                                                                                                                                                          Sequence 46, Application US/08691563C; Patent No. 6001987; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 57.6
Matches 257; Conservative
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STRANDEDNESS: single
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Y: U.S.A.
                                                                                                                                                                                                      CA 8203
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                                                                                                                                                                                                                                                                                                       RESULT 22
US-08-691-563C-46
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DATABASE ENTRY DATE:
DATABASE ENTRY DATE: 1996-01-26
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9.6%; Score 142.4; DB 4;
Best Local Similarity 55.4%; Pred. No. 7.2e-35;
Matches 300; Conservative 0; Mismatches 236;
                                                                                                                                                                                                                                                  APPLICANT: JOAN, KNOLL
APPLICANT: ROGAN, PETER
TITLE OF INVENTION: SINGLE COPY GENOMIC FILE REFERENCE: 30307
CURRENT APPLICATION NUMBER: US/09/573,080A
CURRENT FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 479
1925 TTCAGGCCATAAAGCTCCAGACG 1947
                                                                                                                                      Sequence 26, Application US/09573080A Patent No. 6828097 GENERAL INFORMATION:
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LOCATION: (1)...(8399)
OTHER INFORMATION: herv9
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
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SEQ ID NO 26
LENGTH: 8399
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TITLE OF INVENTION: VIRAL MATERIAL AND NUCLECTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHY
THERAPEUTIC PURPOSES
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                                                                                       1036 TICTACTACAAACTATCTCAAGAAATAAATGGTGACATGGAACAGGTCACTGACTCCCTG
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9
    Indels
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    183;
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NAME: BERRIOGS, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
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REPLICATION UNMERS: US/08/979,847B
FILING DATE: 26-No. 6582703-1997
CLASSIFICATION: <unknown>
    Mismatches
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CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MANDRAND, BERNARD
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JOLIVET-REYNAUD,
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BESEME, FREDERIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 22320
COMPUTER READABLE FORM:
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         Matches 257; Conservative
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ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT
THERAPEUTIC PURPOSES
             1216 TATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAAATTCGAGATCGAATA 1275
                                                                                                                                                                                            1276 CAATGTAGAGCAGAGGAGCTTCAAAACACCGAACGCTGGGGCCTCCTCACCAATGGATG 1335
                                                                                                                                                                                                                                                                          1332 ICTGAAATCAGACAACGCCTTTCAAATTC-----CTATACCAACCTCGGAGTTGGGCA 1385
                                                                                                                                                                                                                                                                                                                                                                          1316 CCCTGGGTTCTCCCCCTTCTTAGGACCTCTAGCAGCTCTAATATTGTTACTCCTCTTTTGGA 1395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1396 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATTGAAGCTGTAAAGCTA 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1272 CTTTACACTAACCAGTCAGGGATAGTATGAGATGCTGCCGGCATTTACAGAAAAGGCT
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ADDRESSEE: Oliff & Berridge
STREET: 700 South Washington Street, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 131.2; DB 4, Pred. No. 1.2e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1456 CAGATGGTCTTACAAATGGAACCCCA 1481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGATGGTCTTACAATGGAACCCCA 1531
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APPLICATION NUMBER: US/08/691,563
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Frederic BEDIN
Glaucia PARANHOS-BACCALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/374,766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 46, Application US/09374766
Patent No. 6579526
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REGISTRATION NUMBER: 30,025
REFERENCE/DOCKET NUMBER: WI
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
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Bernard MANDRAND
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APPLICANT: Bernard M
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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OPERATING SYSTEM:
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Best Local Similarity
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APPLICANT: Herve
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APPLICANT:
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AGTACCCATTCTTCTTTGTTATCAGAGCAGGAGTGCTAGGCAGACTAGGTACTGGCAT 1010
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APPLICANT: CALVERT, JAY G.
APPLICANT: CALVERT, JAY G.
APPLICANT: YANGIDA, NOBORU
TITLE OF INVENTION: VACCINE COMPRISING FOWLPOX VIRUS
TITLE OF INVENTION: RECOMBINANTS EXPRESSING THE ENVELOPE GLYCOPROTEIN OF
TITLE OF INVENTION: AVIAN RETICULOENDOTHELIOSIS RETROVIRUS
CORRESPONDENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                        MAME/KEY: misc binding

LOCATION: 484..502

OTHER INFORMATION: 12-5-158.misl

NAME/KEY: misc binding

LOCATION: 504..523

OTHER INFORMATION: 12-5-158.mis2, potential complement

NAME/KEY: primer bind

LOCATION: 346..366

OTHER INFORMATION: upstream amplification primer

NAME/KEY: primer bind

COTHER INFORMATION: downstream amplification primer

NAME/KEY: misc binding

LOCATION: 491..515

OTHER INFORMATION: 12-5-158 potential probe

NAME/KEY: misc feature

LOCATION: 314,336,793

COTHER INFORMATION: n=a, g, c or t

US-09-671-317-406
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                                                                                                                                                                                                    LOCATION: 503
OTHER INFORMATION: 12-5-158 : polymorphic base C or
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Pred. No. 1.8e-31;
0; Mismatches 99;
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8110 Gatehouse Road Suite 500 East
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Patent No. 5403582
GENERAL INFORMATION:
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Best Local Similarity 67.6%;
Matches 211; Conservative 0
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                                                                      TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                    NAME/KEY: allele
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US-08-007-282B-1
SEO ID NO 406
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| Sequence 406, Application US/09671317
| Patent No. 6528260
| GENERAL INFORMATION:
| APPLICANT: Blumenfeld, Marta
| APPLICANT: Blumencov, Ilya
| APPLICANT: Chumakov, Ilya
| APPLICANT: Chumakov, Ilya
| APPLICANT: Chumakov, Ilya
| APPLICANT: Cohen, Annick
| TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
| TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
| TITLE OF INVENTION: BIALLELIC MARKERS PORTON OF 2.7
| CURRENT APPLICATION NUMBER: US 99/536,178
| PRIOR PILING DATE: 2000-03-23
| PRIOR PILING DATE: 2000-03-24
| PRIOR APPLICATION NUMBER: US 60/126,269
| PRIOR FILING DATE: 1999-03-25
| PRIOR FILING DATE: 1999-04-36
| PRIOR FILING DATE: 1999-04-36
| WUMBER OF SEQ ID NOS: 977
| WUMBER OF SEQ ID NOS: 977
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Pred. No. 1.2e-31;
0; Mismatches 183;
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       TELECOMMUNICATION INFORMATION:
                                                                                                  INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 1859 base pairs
                                          TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 57.6%;
Matches 257; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 21526;
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Pred. No. 2.8e-26;
0; Mismatches 217; Indels
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Best Local Similarity 54.2%;
Matches 260; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 14685
LENGTH: 21526
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                                                                                                                    COMPUTER:

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COMPUTER:

COPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Parentin Release #1.0, Version #1.25

SOFTWARE: Parentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/007,282B

FILING DATE: 19930121

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: MURPHY JR., GERALD M.

REGISTRATION NUMBER: 1644-104P

TELECOMMUNICATION NUMBER: 1644-104P

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFHONE: 703-205-8000
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7.9%; Score 116.8; DB 1
Best Local Similarity 51.5%; Pred. No. 5.8e-27;
Matches 268; Conservative 0; Mismatches 15.
                                                                                                             3: Floppy disk
IBM PC compatible
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1704 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
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                                                                                     COMPUTER READABLE FORM:
Falls Church
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                                             COUNTRY:
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Sequence 14685, Application US/09949016

Sequence 14685, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

NUMBER OF SEQ ID NOS: 207012
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SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATI
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                               AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A TITLE: Prototypic sequences for human repetitive DNA JOURNAL: Journal of Molecular Evolution VOLUME: 35 USUE: 4 PAGES: 286-291 DATE: 1992-10-
                                                                                                                                                                                                                                                                                                                                                                                                  7.8%; Score 115.2; DB 4;
54.0%; Pred. No. 5e-26;
tive 0; Mismatches 218;
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US-09-573-080A-44
; Sequence 44, Application US/09573080A
; Patent No. 6828097
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOLL;
; APPLICANT: ROGAN, PETER
; TILLE OF INVENTION: SINGLE COPY GENOMIC HYBE
; FILE REFERENCE: 30307
; CURRENT PELLING DATE: 2000-05-16
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SOFTWARE: Patentin version 3.0
SEQ ID NO 44
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NAME/KEY: repeat region
LOCATION: (1)..(7392)
OTHER INFORMATION: hervr
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 54.0
Matches 259; Conservative
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      PUBLICATION INFORMATION
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US-09-573-080A-30
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APPLICANT: MCGAN, PETER
TITLE OF INVENTION: BTER
TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATI
FILE REPERENCE: 30307
CURRENT APPLICATION NUMBER: US/09/573,080A
CURRENT FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 479
SSOFTWARE: Patentin version 3.0
LENGTH: 7713
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Pred. No. 3.5e-27;
1; Mismatches 175;
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FABELSEQ for Windows Version 4.0
SEQ ID NO 194497
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US-09-573-080A-30
Sequence 30, Application US/09573080A
Patent No. 6828097
GENERAL INFORMATION:
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Query Match
Best Local Similarity 58.5%
Matches 257, Conservative
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NAME/KEY: repeat region
LOCATION: (1) . (7713)
OTHER INFORMATION: hervh
PUBLICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Human
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                                                                                   349 AGTACTCCCAGTCCATACAAGAAATTAGACCTTTCCAGGCTACAGGAARCCCTTAACTCT
                                                                                                                                                     CATACTCGCCTGGTGAGCCTATTTAATACCACCTCACGGCTCCATGAGGTCTCAGCC
                        AGCACCCCTAGCCCCTACAAAGGACTAGTTCTCTCAAAACTACATGAAACCCTCCGTACC
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Pred. No. 2.9e-25;
0; Mismatches 202;
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APPLICANT: Du Sart, Desiree
APPLICANT: Du Sart, Desiree
APPLICANT: Du Sart, Desiree
APPLICANT: Du Sart, Desiree
FILE REPERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 55.7'
Matches 263; Conservative
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LENGTH: 80246
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                                                                                                                                          ISSUE: 4
PAGES: 286-291
DATE: 1992-10-
DATABASE ACCESTON NUMBER: Database of repetitive elements (repbase)
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DATABASE ENTRY DATE:
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND VETLE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A TITLE: Prototypic sequences for human repetitive DNA JOURNAL: Journal of Molecular Evolution
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Pred. No. 1.4e-26;
1; Mismatches 128;
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Pred. No. 5.6e-26;
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 56.9%;
Matches 211; Conservative
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Best Local Similarity 61.8
Matches 215; Conservative
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FACERAL INCEMATION:
APPLICANT: Collins, Mary KL
APPLICANT: Collins, Mary KL
APPLICANT: Weise, Robin A
APPLICANT: Cosset, Francols-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT PRILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1996-08-23
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
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RESULT

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2752 CAAGACCAGGTAGATCTGGTTAGCTGAAGTAGTTCTCCAAAATAGGAGGGGACTGGACCTA 2811
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OTHER INFORMATION: Description of Artificial Sequence: Portion of
OTHER INFORMATION: construct
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Pred. No. 8.8e-26;
0; Mismatches 183;
                                                        APPLICANT: COllins, Mary KL
APPLICANT: Weiss, Robin A
APPLICANT: Weiss, Robin A
APPLICANT: Weiss, Robin A
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT FILING DATE: 1998-06-22
CURRENT FILING DATE: 1998-06-23
EARLIER APPLICATION WUMBER: PCT/GB96/02061
EARLIER APPLICATION NUMBER: CT/GB96/02061
EARLIER APPLICATION NUMBER: GB9517263.1
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 8
SEQ ID NO 9
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!LOCATION: (3802)
| OTHER INFORMATION: n is any nucleotide
| US-09-011-745-8
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NOME/KEY: misc feature
LOCATION: (3611)
OTHER INFORMATION: n is any nucleotide
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Sequence 8, Application US/09011745, Patent No. 6165715, GENERAL INFORMATION:
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Best Local Similarity 55.0%;
Matches 224; Conservative (
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LOCATION: (3801)
OTHER INFORMATION: n is
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LOCATION: (3612)
OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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NAME/KEY: misc_feature
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LOCATION: (3614)
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Sequence 1, Application US/0955352

Patent No. 6544779

GENERAL INFORMATION:
APPLICANT: Cichutek, Klaus

TITLE OF INVENTION: PSEUDO-TYPE RETROVIRAL VECTORS WITH
TITLE OF INVENTION: PSEUDO-TYPE RETROVIRAL VECTORS WITH
TITLE OF INVENTION: PSEUDO-TYPE RETROVIRAL VECTORS WITH
TITLE OF INVENTION: PSEUDO-TYPE RETROVIRAL VECTORS WITH
TITLE OF INVENTION: PSEUDO-TYPE RETROVIRAL VECTORS WITH
TITLE OF INVENTION: PSEUDO-08-24

CURRENT FILING DATE: 1692-005001

PRIOR FILING DATE: 1998-11-27

PRIOR FILING DATE: 1998-11-27

PRIOR FILING DATE: 1997-11-28

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 3.5e-25;
0; Mismatches 243;
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ORGANISM: Murine leukemia virus
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Best Local Similarity 51.5<sup>†</sup>
Matches 258; Conservative
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CTAACGGCAGAACAAGGAGGAATTTGTTTAGCCTTACAAGAAAAATGCTGTTTTTATGCT 2871
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                                                                                                                                                                                                                              2932 Agggaangcchggcaaaccaactachchgaccggchgcagggartrchtcchacchc
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                                                             1225 AATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAAATTCGAGATCGAATACAATGTAGA
                                                                                                                    AACAAGTCAGGAATTGTGAGAAACAAAATAAGAACCCTACAAGAAGAATTACAAAAAACGC
                                                                                                                                                                              1285 GCAGAGGAGCTTCAAAACACCGAACGCTGGGGCCTCCTCAGCCAATGGATGCCCTGGGTT
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Pred. No. 3.1e-25;
0; Mismatches 224; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 28, Application US/09573080A
Patent No. 6828097
GENERAL INFORMATION:
APPLICANT: JOAN, KNOLL
APPLICANT: ROGAN, PETER
TITLE OF INVENTION: SINGLE COPY GENOMIC HYB
FILE REFERENCE: 33307
CURRENT FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 479
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Best Local Similarity 54.3%;
Matches 274; Conservative
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LOCATION: (1)...(5529)
OTHER INFORMATION: hervfh21
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
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PAGES: 286-291
DATE: 1992-10-
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US-09-573-080A-28
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US-09-573-080A-28
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SEQ ID NO 28
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2031 GAAAGGGGGTACCTGCATATACCTCCAGGAAGAATGCTGTTTCTGTGTTAATGAATCTGG 2090
                                                                                                             2091 cárricircararcecaerriceraeecrricareaeecrecaeaecrraeacarcaaer 2150
                                                                                                                                                       GCTTCAAAACACCGAACGCTGGGGGCCTCCTCAGCCAATGGATGCCTGGGTTCTCCCCTT 1352
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                                                                   1236 AATTGTCACTGAGAAAGTTAAAGAAATTCGAGATCG---AATACAATGTAGAGCAGAGA
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Pred. No. 5.7e-23;
0; Mismatches 187;
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/09904615
Sequence 12, Application US/09904615
Sequence 12, Application US/09904615
GENERAL INFORMATION:
TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: PZ032P1
CURRENT APPLICATION NUMBER: US/09/904,615
CURRENT FILING DATE: 2001-07-16
PRIOR FILING DATE: 2000-02-23
PRIOR FILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 170
SOSTWARE: PATENTING UNCE: 2.0
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Best Local Similarity 54.8%;
Matches 230; Conservative
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US-09-904-615-12
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                                     CTGGGGCCTCCTCAGCCAATGCATGCCCTGGGTTCTCCCCTTTAGGACCTCTAGCAGC 1370
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TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypebtides
FILE REPERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312B
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-01-21
PRIOR PILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PL_genes Version 1.0
SEQ ID NO 171
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                                                                                                                                                                                                                                                                                                                                                                      Sequence 171, Application US/09620312D Patent No. 6569662 GENERAL INFORMATION:
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Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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APPLICANT: Tang, Y. Tom
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Chen, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Xue, Aidong J.
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Zhou, Ping
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US-09-620-312D-171
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US-09-620-312D-171
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LOCATION: (19:
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Patent No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                       GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307

CORRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PastSEQ for Windows Version 4.0
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Pred. No. 1.5e-21;
0; Mismatches 211; Indels
Sequence 12735, Application US/09949016
Patent No. 6812339
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16; Conservative
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US-09-949-016-13572/c
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LENGTH: 80355
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Pred. No. 1.5e-21;
0; Mismatches 211;
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SQ THARE: FBSEG for Windows Version 4.0
SQ ID NO 13572
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al Similarity 53.1%;
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Matches 246; Conserv
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US-09-949-016-13572
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10694.149 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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                                                                                                                                                                                                                                                 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	% Query Match Length DB ID	DB	CI	Description	į
	1481		:	89	8 US-08-979-847-105	Sequence 105, App	App
8	1481			16	US-10-114-104-105	Sequence 105,	, App
m	1481			17	US-10-637-565-18	Sequence 18,	Appl
4	1389.8			17	US-10-416-642-4	Sequence 4, Appli	Appli
5	1335.4			σ	US-09-902-535-1	Sequence 1, Appli	ppli
9	1335.4			13	US-10-114-893-134	Sequence 134, App	, App
7	1335.4			12	US-10-016-249-3	Sequence 3, A	Appli
8	1333.8	90.1	1617	17	17 US-10-133-036-3	Sequence 3, Appli	Appli
9	1333.8			10	US-09-854-867-21	Sequence 21,	Appl
10	1333.8		56093	10	US-09-873-367C-81	Sequence 81,	App1
11	1324.2			17	US-10-632-793-30	Sequence 30,	Appl

Sequence 1, Appli	Sequence 26, Appl	_	444	Seguence 24, Appl	Seguence 21192, A	Sequence 228, App	Sequence 19, Appl	Sequence 25, Appl	Sequence 23, Appl	Sequence		Sequence	Sequence	Seguence	Sequence		Sequence	Sequence 32257	Sequence 139	Sequence 108,	Sequence 108, App	Sequence 1403	2	2 Sequence	Sequence 86541,		7501,	Seguenc	Seguence 7	Seguence	Sequence 1500	Sequence 8521	Sequence
US-10-133-036-1	US-10-632-793-26	US-10-087-192-730	US-09-864-761-4444	US-10-632-793-24	Þ	US-10-363-616-22	US-10-632-793-19	US-10-632-793-2	US-10-632-793-2		US-10-027							US-10-027-632-322575		US-08-979-847-108	US-10-114-104-108	US-09-864-761-14030			US-10-027-632-865		US-09-864-761-7501	US-10-029-386-20259	US-09-864-761-7310	₽	US-10-027-632-1500	US-10-027-632-8521	US-1
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1308.2	1306.6	1277.4	1131.6	1116.4	716.6	591.8	582.8	516.6	513.6	377.8	377.8	377.8	377.8	364	353	353	353	353	318.6	302	302	296	229.8	229.8	229.6	229.6	219.4	213	194.8	189.8	189.8	173.8	
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ALIGNMENTS

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US-08-97-847-105
| Sequence 105, Application US/08979847
| Publication No. US20030039664A1
| GENERAL INFORMATION:
| APPLICANT: PERENCH |
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| APPLICANT: PERENCH |
| APPLICANT: PARANHOS-BACCALA, GLAUCIA |
| APPLICANT: PARANHOS-BACCALA, GLAUCIA |
| APPLICANT: PARANHOS-BACCALA, GLAUCIA |
| APPLICANT: PARANHOS-BACCALA, GLAUCIA |
| APPLICANT: USEN |
| APPLICANT: USEN |
| APPLICANT: USEN |
| APPLICANT: WAUDRAND, BERNAD |
| APPLICANT: TUKE, PHILLF |
| TITLE OF INVENTION: THERAPEUTIC PURPOSES |
| TITLE OF INVENTION: THERAPEUTIC PURPOSES |
| TITLE OF INVENTION: THERAPEUTIC PURPOSES |
| TITLE OF INVENTION: THERAPEUTIC PURPOSES |
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| MEDIUM TYPE: Floppy disk |
| COMPUTER READABLE
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TUKE, PHILL MATERIAL AND NUCLEOTIDE FRAGMENTS
OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYI
THERAPEUTIC PURPOSES
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BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
JOLIUET-REYNAUD, COLETTE
MANDRAND, BERNARD
GARSON, JERENY
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CORRESPONDENCE ADDRESS:
ADDRESSE: OLIFF & BERRIDGE, PI
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 105, Application US/10114104
Publication No. US20030198647A1
GENERAL INFORMATION:
APPLICANT: PERRON, HERVE
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US-10-114-104-105
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; Pred. No. 0;
0; Mismatches
                                             39046A
     ATTORNEY/AGENT INFORMATION:

NAME: BERRIDGE, WILLIAM P.

REGISTRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: 30,024

REFERENCE/DOCKET NUMBER: WB 390

TELECOMMUNICATION INFORMATION:

TELECHONE: 703-836-2787

INFORMATION FOR SEQ ID NO: 105:

SEQUENCE CHARACTERISTICS:

LENGTH: 1481 base pairs

TYPE: nucleic acid

STRANDEDNESS: 81ngle

TYPE: nucleic acid

STRANDEDNESS: 81ngle

STRANDEDNESS: 81ngle

STRANDEDNESS: 81ngle

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Best Local Similarity 100.0%;
Matches 1481; Conservative 0;
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RESULT 3

US-10-637-565-18

US-10-637-565-18

US-10-637-565-18

US-10-637-565-18

Subjication No. US20040043381A1

GENERAL INFORMATION:

APPLICANT: PARANHOS-BACCALA, Glaucia:

APPLICANT: KOMURIAN-PRADEL, Florence

APPLICANT: KOMURIAN-PRADEL, Florence

TITLE OF INVENTION: THE LIR REGION OF MSRV-1 AND THE PROTEINS IT ENCODES, AND PROBES

TITLE OF INVENTION: METHODS FOR DETECTING MSRV-1 RETROVIRUS

FILE REPERBENCE: 110257

CURRENT APPLICATION NUMBER: US/10/637,565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1440
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               ATAGICTGCCTACCCTCAGGAATATTTTTGTCTGTGGTACCTCAGCCTATCATTGTTTG
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                                                       Version
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NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 105:
     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/114,104
FILING DATE: 03-Apr-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1481;
100.0%; Pred. No. 0;
tive 0; Mismatches
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MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-114-104-105
                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,847
FILING DATE: 26-NOV-1997
                                                                                                                                                                                                                                                            LENGTH: 1481 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 1481; Conservative
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ORGANISM: Homo sapiens
PEATURE:
PEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20040043452Al 7477736CBl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/10416642;
Publication No. US20040043452A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: ARVIZU, Chandra
ITLE OF INVENTYOR: EMERYOGENESIS ASSOCIATED PROTEINS
FILE REFREENCE: PF-0842 PCT
CURRENT APPLICATION NUMBER: US/10/416,642
CURRENT FILING DATE: 2003-05-13
PRIOR APPLICATION NUMBER: 60/249,407
PRIOR APPLICATION NUMBER: 60/249,407
PRIOR FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 4
LENGTH: 2074
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                                                                                                                                                                                                                                                           ; Score 1481; E
; Pred. No. 0;
0; Mismatches
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: US/09/890,340
PRIOR FILING DATE: 2001-11-27
PRIOR FILING DATE: 2000-02-15
PRIOR FILING DATE: 2000-02-15
PRIOR REPLICATION NUMBER: EP 99420041.8
PRIOR PRIOR PILING DATE: 1999-02-15
NUMBER OF SEQ ID NOS: 20
SEQ ID NOS: 20
SEQ ID NO 18
                                                                                                                                                                                                                                                           Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 1481; Conservative 0
                                                                                                                                                           TYPE: DNA ORGANISM: MSRV-1 retrovirus
                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (1)..(1626)
US-10-637-565-18
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Pred. No. 0;
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; LOCATION: (930)...(2546)
US-09-902-535-1
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Best Local Simi
Matches 1390;
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Pred. No. 0;
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Best Local Similarity 96.2%;
Matches 1424; Conservative
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; FEATURE:
; NAME/KEY: unsure
; LOCATION: 1995
; OTHER INFORMATION: a, t,
US-10-416-642-4
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	RESULT 6 US-10-114-893-134 Sequence 134, Application US/10114893 Sequence 134, Application US/10114893 Sequence 134, Application No. US20020193567A1 GENERAL INFORMATION: APPLICANT: Jacobs, Kenneth APPLICANT: LaVallie, Edward R. APPLICANT: Evans, Cheryl APPLICANT: Evans, Cheryl APPLICANT: Paward, Maurice APPLICANT: Spaulding, Vikia APPLICANT: Spaulding, Vikia APPLICANT: Kelleher, Kerry S. APPLICANT: Garlin-Duckett, McKeough APPLICANT: Garlin-Duckett, McKeough APPLICANT: Garlin-Duckett, Inc. TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING TITLE APPLICANTON: DATE: 2,002-04-02	CORRIGE APPLICATION NUMBER: 09/413,232
61 GCACCCCTCCATGCTGCTACCAGCAGCTACCAAGCAGTTTCTATGAAGA 120	AGACCCCTAGCCCTAGAAGGACTAGTTCTCTCAAAACTAGAAACCCTCCGTAGC aGCACCCTGCCCTAGAAGGACTAGTTCTCTCAAAACTAGAAACCCTCCGTACC aGCACCTTGCCTGGCCCTAAAGGACTAGATCTCTCAAAACTACATGAAACCCTCCGTACC catactcGcCTGGTAGCCTATTTAATACCACCCTCACTGGGCTCCATGAGGTCTCAGCC catactcGcCTACTAGTTGGATGTGCCTCCCCTCACTGGGCTCCATGAGGTCTCAGCC catactcGcCTACTAACTGTTGGATGTGCCTCCCCTCACTGGGCTCCATGAGGTCTCAGCC catactcGCTACTAACTGTTGGATGTGCCTCCCCTGCACTTCAGGCCATATTTAATACACCTTCCTACTAGACTTTCAATC catactcGCTACTAACTGTTGGATATGCCTCCCCCTGAACTTCAGGCCATATTTAATA ccTGTTCCTGAACAATGGAAATAGCACACAGAAATAAACACCACTTCCGTTTTAGTA ccTGTTCCTGAACAATGGAAATAACCCACAAACTTCCGTTTTAGTA ccTGTTACTTTCCAATCTGGAAATAACCCACAACCTCACACTTCCGTTTTAGTA GGACCTCTTGTTTCCAATCTGGAAATAACCCCTAAACTCACACCTGTGTAAAATTT GGACCTCTTGTTTCCAATCTGGAAATAACCCCTAAACCTCACCTGTGTAAAATTT GGACCTCTTGTTTCCAATCTGGAAATAACCCCTAAACCTCACCTGTGTAAAATTT GGACCTCTTGTTTCCAATCTGGAAATAACCCCTAAACCTCACCTGTGTAAAATTT GGACCTCTTGTTTCCAATCTGGAAATAACCCCTAAACCTCACCTGTGTAAAATTT GGACCTCTTGTTTCCAATCTGGAAATAACCCCTAACCTCACACTGTGTAAAATTT GGACCTCTTGTTTCCAATCTGGAAATAACCCCTAAACCTCACCTGTGTAAAAATTT GGACCTCTTGTTTCCCAATCTGGAAATAACCCCTAAACCTCACCTGTGTAAAAATTT GGACCTCTTGTTTCCCAATCTGGAAATAACCCCTAACCTCACTGTGTAAAAATTT GGACCTCTTGTTTCCCAATCTGGAAATAACCCCCAAACCTCACCTGTGTAAAAATTT GGACCTCTTGTTTCCCAATCTGGAAATAACCCCAAACCTCACTGTGTAAAAATTT GGACCTCTTGTTTCCCAATCTGGAAATAACCCCAAACCTCACCTGTGTAAAAATTT GGACCTCTTGTTTCCCAATCTGGAAATAACCCCAAACCTCACCTGTGTAAAAATTT GGACCTCTTGTTTCCAATCTGGAAATAACCCCAAACCTCACCTGTGTAAAAATTT GGACCTCTAACTACTACTACTACAACCTCACCTGTGTAAAAATTT GGACCTCTCAAACTCTAAAAAAAAAA	721 AGCALTACTATAGACCACCCATGCATCAGTGGGTAACCTCCCACACAGA 780 1650 AGCATACTACACAACCAACCCATCCCATCGATCGGTAACCTCCCACACAGA 780 1650 AGCATACTACACAACCAACCAACCATCCCATCGATCAGTGGGTAACCTCCCACACAA 1709 781 ATAGTCTGCCTACCCTCAGGATATTTTTTTTTTTTTTTT

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                                                      APPLICANT: Corrad, Bernard
APPLICANT: Corrad, Bernard
TITLE OF INVENTION: Multiple Sclerosis-Related Superantigen
TITLE OF INVENTION: Multiple Sclerosis-Related Superantigen
FILE REFERENCE: 23135-507
CURRENT APPLICATION NUMBER: US/10/133,036
CURRENT FILING DATE: 2002-04-26
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
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Pred. No. 0;
0; Mismatches
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               ; Sequence 3, Application US/10133036; Publication No. US20040054133A1; GENERAL INFORMATION: APPLICANT: Conrad, Bernard
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Best Local Similarity 93.8
Matches 1389; Conservative
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           GCCACCTCTAGCCCCTACAAAGGACTAGATCTCTCAAAACTACATGAAACCCTCCGTACC
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Best Local Similarity 93.8%; Pred. No. 0;
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APPLICANT: NOGAN, RETER K
TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF
FILE REFERENCE: 30307
CURRENT APPLICATION NUMBER: US/09/854,867
CURRENT APPLICATION NUMBER: 203.05-08
NUMBER OF SEQ ID NOS: 6110 N
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| APPLICANT: Young, Paul |
| APPLICANT: Soppet, Daniel |
| APPLICANT: Soppet, Daniel |
| APPLICANT: Endress, Gregory |
| APPLICANT: Endress, Gregory |
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| APPLICANT: Endress, Gregory |
| APPLICANT: Endress, Gregory |
| APPLICANT: Carter, Kenneth |
| TITLE OF INVENTION: Signature Gene Sets |
| FILE REPRENCE: 689220-64 |
| FILE REPRENCE: 689220-64 |
| CURRENT APPLICATION NUMBER: U.S. 60/236,891 |
| PRIOR APPLICATION NUMBER: U.S. 60/236,892 |
| PRIOR FILING DATE: 2000-09-29 |
| PRIOR FILING DATE: 2000-01-01 |
| PRIOR FILING DATE: 2000-11-01 |
| PRIOR FILING DATE: 2000-11-01 |
| PRIOR FILING DATE: 2000-11-01 |
| NUMBER OF SEQ ID NOS: 1067 |
| SOFTWARE: Patentin version 3.0 |
| SEQ ID NO 81
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Best Local Similarity 93.8%;
Matches 1389; Conservative C
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ORGANISM: Homo sapiens
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92.2%; Pred. No. 0;
tive 24; Mismatches
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NAME/KEY: misc feature
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... OTHER INFORMATION: n = a or g or c or t/u
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Best Local Similarity 92.2%
Matches 1365; Conservative
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NAME/KEY: misc_feature
LOCATION: (3787)..(3787)
OTHER INFORMATION: n = a
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NAME/KEY: misc_feature
LOCATION: (4115)..(4115)
OTHER INFORMATION: n = a
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NAME/KEY: misc_feature
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                    LOCATION: (2213)..(2213)
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GENERAL INVORTATION:

APPLICANT: PARANHOS-BACCALA, Glaucia
APPLICANT: WALLET, Francois
APPLICANT: VOISSET. Cecile
TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN
TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN
TITLE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT
FILE REFRENCE: 110048
CURRENT APPLICATION NUMBER: US/09/869,927
FRIOR APPLICATION NUMBER: US/09/869,927
FRIOR APPLICATION NUMBER: FF 99/00688
FRIOR FILING DATE: 2001-10-22
FRIOR FILING DATE: 2000-01-21
FRIOR APPLICATION NUMBER: FF 99/00688
FRIOR FILING DATE: 1999-01-21
FRIOR FILING DATE: 1999-01-21
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Sequence 730, Application US/10087192

GENERAL INFORMATION:

APPLICANT: MORTIA, David W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CURRENT APPLICATION CAMCER.

FILE REFERENCE: 529452000122

CURRENT APPLICATION NUMBER: US/10/087,192

CURRENT APPLICATION NUMBER: US 09/747,377

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2001-103-05

SOFTWARE: FABELSEQ for Windows Version 4.0

SEQ ID NO 730

TEMPORE: CALLOS APPLICATION NOT 300
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; OTHER INFORMATION: n = A,T,C or US-10-087-192-730
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Best Local Similarity 92.5%;
Matches 1399; Conservative
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  ; OTHER INFORMATION: E
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Sequence 4444, Application US/9864761

SEPECENT NO. US/9020048753A1

SERVERAL INFORMATION:

PREPLICANT: Rent, Sharich G.

PREPLICANT: Henrel, David K.

APPLICANT: Henrel, David K.

APPLICANT: The WESTROWN WESTROWN WESTROWN WICKELC ACID PROBES USEFUL FOR TITLE OF INVERTION: HURNAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVERTION: USER SOLID SINGLE S
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                                                               TYPE: DNA
ORGANISM: Homo sapiens
PEATURE:
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 6
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.4
OTHER INFORMATION: EXPRESSED IN BEART, SIGNAL = 5.9
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Sequence 24, Application No. US20040048298A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PARANHOG-BACCALA, Glaucia
APPLICANT: PARANHOG-BACCALA, Glaucia
APPLICANT: WALLET, Francois
APPLICANT: VOISSET, Cecile
TITLE OF INVENTION: AUTOHMUNE DISBASE, LABELING METHOD AND REAGENT
TITLE OF INVENTION: AUTOHMUNE DISBASE, LABELING METHOD AND REAGENT
TITLE OF INVENTION: AUTOHMUNE DISBASE, LABELING METHOD AND REAGENT
TITLE OF INVENTION: AUTOHMUNE DISBASE, LABELING METHOD AND REAGENT
CURRENT APPLICATION NUMBER: US/10/632,793

CURRENT FILING DATE: 2003-08-04
PRIOR FILING DATE: 2000-01-21

PRIOR FILING DATE: 2000-01-21

PRIOR FILING DATE: 1999-01-21

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PATCHTON NUMBER: FF 99/0088

PRIOR FILING DATE: 1999-01-21

NUMBER OF SEQ ID NOS: 33

SEQ ID NO 24

LENGTH: 1948
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LOCATION: (84)...(84)
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FEATURE:
LOCATION: (1937)...(1933)
OTHER INFORMATION: n = a OX
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EXPRESSED IN HELA, SIGNAL = 7.2
MT HIT: AF208161.1, EVALUE 0.00e+00
EST HUMAN HIT: AU138405.1, EVALUE 0.00e+00
SWISSPROT HIT: P10269, EVALUE 2.00e-16
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Pred. No. 1.4e-209;
0; Mismatches 39;
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US-10-363-616-228
; Sequence 228, Application US/10363616
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APPLICANT: Penn, Sharten G.
APPLICANT: Bank, David R.
APPLICANT: Bank, David R.
APPLICANT: Bank, David R.
APPLICANT: HURCHARITION
TITLE OF INVENTION: GIBE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GIBE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: AGOING B.
TITLE OF INVENTION NUMBER: US/09/864,761
CURRENT FILING DATE: 2000-02-04
PRIOR PALLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2000-02-04
PRIOR PALLICATION NUMBER: US/09/864,765
PRIOR PALLICATION NUMBER: US/09/864
PRIOR PALLICATION NUMBER: US/09/864
PRIOR PALLICATION NUMBER: US/09/866
PRIOR PALLICATION NUMBER: US/09/866
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                                               CAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTA
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC002146.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 20
OTHER INFORMATION: EXPRESSED IN HELLO, SIGNAL = 6
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.4
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 5.9
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 5.9
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0
                                                                                                                       GGAGAAGAACGCTGTTATTATGTTAATCAA 1230
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Patent No. US20020048763A1
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Best Local Similarity 98.8%; Pred. No. 6.2e-171;
Matches 596; Conservative 0; Mismatches 7; Indels 0;
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hyeaq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POL.
FILE OF INVENTION: NOVEL NUCLEIC ACIDS AND POL.
CURRENT APPLICATION NUMBER: US/10/363,616
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 09/654,935
PRIOR FILING DATE: 2000-09
NUMBER OF SEQ ID NOS: 490
SEQ ID NO 228
LENGTH: 1684
                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                         ; LOCATION: (89)..(1684)
US-10-363-616-228
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NAME/KEY: CDS
LOCATION: (89)
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RESULT 19
US-10-632-793-19
US-10-632-793-19
, Sequence 19, Application US/10632793
, Publication No. US20040048298A1
, GENERAL INFORMATION:

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APPLICANT: PARANHOS-BACCALA, Glaucia
APPLICANT: MALLET, Francois
APPLICANT: WALLET, Francois
APPLICANT: VOISSET, Cecile
TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN
TITLE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT
FILE REFERENCE: 110048
CURRENT APPLICATION NUMBER: US/10/632,793
CURRENT FILING DATE: 2003-08-04
PRIOR FILING DATE: 2003-10-22
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
SPRIOR FILING DATE: 2000-01-21
SPRIOR FILING DATE: 2000-01-21
SPRIOR FILING DATE: 2000-01-31
SOFTWARE: PALENTING DATE: 1999-01-21
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PALENTIN VERSION 3.1
LENGTH: 591
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Pred. No. 2e-168;
0; Mismatches 2; Indels
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; Sequence 25, Application US/10632793
; Fublication No. US20040048298A1
; FUBLICATION: APPLICANT: PARANHOS-BACCALA, Glaucia
                                                                                                                                                                                                                                                                                                                                                                                             39.4%;
                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 99.7 Matches 584; Conservative
                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-632-793-19
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APPLICANT: MALLET, Francois
APPLICANT: VOISSET, Cecile
TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN
TITLE OF INVENTION: BUDGOENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN
TITLE OF INVENTION: AUTOIMMURE DISEASE, LABELING METHOD AND REAGENT
FILE REFERENCE: 110048
CURRENT APPLICATION NUMBER: US/10/632,793
CURRENT APPLICATION NUMBER: US/09/869,927
PRIOR FILING DATE: 2000-10-22
PRIOR FILING DATE: 2000-10-21
PRIOR FILING DATE: 1999-01-21
PRIOR FILING DATE: 1999-01-21
PRIOR FILING DATE: 1999-01-21
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.1
SEQ ID NO 25
LENGTH: LING
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Score 516.6; DB 17;
Pred. No. 7.5e-148;
0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 34.9%;
Best Local Similarity 91.8%;
Matches 546; Conservative (
                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-10-632-793-25
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Sequence 23, Application US/10632793
Publication No. US20040048298A1
GENERAL INFORMATION:
APPLICANT: PARANMOS-BACCALA, Glaucia
APPLICANT: MALLET, Francois

US-10-632-793-23

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APPLICANT: VOISSET, Cecile
TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN
TITLE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT
FILE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT
FILE REFERENCE: 110048
CURRENT APPLICATION NUMBER: US/10/632,793
CURRENT APPLICATION NUMBER: US/09/869,927
FRIOR APPLICATION NUMBER: PC/FR00/00144
PRIOR PLING DATE: 2000-1.21
PRIOR PLING DATE: 1999-01-21
PRIOR FILING DATE: 1999-01-21
NUMBER OF SEQ ID NOS: 33
SOUTHARE: PALENTIN VERSION 3.1
SEQ ID NO 23
LENGTH: 2006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1540 ATGCAGCGTCCCGGAAATATTGATGCCCCATCGTATAGGAGTCTTTCTAAGGGAACCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 ACCTICACTGCCCACACCCATATGCCCCGCAACTGCTATAACTCTGCCACTCTTTGCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 513.6; DB 17
Pred. No. 8.6e-147;
0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature

) LOCATION: (305)..(305)

) OTHER INFORMATION: n = a or g or c or t/u

US-10-632-793-23
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US-10-027-632-322491/c
Sequence 322491, Application US/10027632
Publication No. US20020198371A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 93.2%;
Matches 548; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Human
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SEQ ID NO 322492
LENGTH: 570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 10827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US/0218,006

PRIOR APPLICATION NUMBER: US 60/118,676

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-04-29

PRIOR FILING DATE: 2000-04-29

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/195,218

PRIOR PELING DATE: 2000-02-24

PRIOR FILING DATE: 1099-11-28

PRIOR FILING DATE: 1999-11-28

PRIOR FILING DATE: 1999-104-08

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-38

PRIOR FILING DATE: 1999-09-38

PRIOR FILING DATE: 1999-09-08

NUMBER OF SEQ ID NOS: 325720

SEQ ID NO 322491

LENGTH: 570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 25.5%; Score 377.8; DB 13; Length Best Local Similarity 90.7%; Pred. No. 3e-105; Matches 411; Conservative 2; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCACCCCTAGCCCCTACAAAGGACTAGTTCTC 453
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US-10-027-632-322491
                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (1)...(570)
                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
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APPLICANT: NAORY David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027.632
CURRENT FILING DATE: 2002-04-30
FRIOR PILING DATE: 2000-07-12
FRIOR PILING DATE: 2000-07-12
FRIOR APPLICATION NUMBER: US 60/198,676
FRIOR FILING DATE: 2000-04-20
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR APPLICATION NUMBER: US 60/165,363
FRIOR FILING DATE: 2000-02-24
FRIOR PILING DATE: 1909-09-28
FRIOR APPLICATION NUMBER: US 60/166,358
FRIOR APPLICATION NUMBER: US 60/166,358
FRIOR APPLICATION NUMBER: US 60/146,002
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-08-09
FRIOR FILING DATE: 1999-08-09
FRIOR FILING DATE: 1999-08-09
FRIOR FILING DATE: 1999-08-09
FRIOR FILING DATE: 1999-08-09
FRIOR FILING DATE: 1999-08-09
FRIOR FILING DATE: 1999-08-09
FRIOR FILING DATE: 1999-08-09
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Pred. No. 3e-105;
2; Mismatches 39; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCACCCTAGACCTACAAAGGACTAATCCCC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | NAME/KEY: misc_feature
| LOCATION: (1)...(570)
| OTHER INFORMATION: n = A,T,C or G
| US-10-027-632-322492
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Best Local Similarity 90.7
Matches 411; Conservative
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RESULT 24 US-10-027-632-322491/c

RESULT 23 US-10-027-632-322492/c ; Sequence 322492, Application US/10027632

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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Oblymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT PELING DATE: 2002-04-30
FRIOR APPLICATION NUMBER: US 60/218,006
FRIOR APPLICATION NUMBER: US 60/218,006
FRIOR APPLICATION NUMBER: US 60/198,676
FRIOR APPLICATION NUMBER: US 60/198,676
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR PILING DATE: 2000-03-29
FRIOR PILING DATE: 2000-03-24
FRIOR APPLICATION NUMBER: US 60/185,218
FRIOR APPLICATION NUMBER: US 60/165,358
FRIOR APPLICATION NUMBER: US 60/166,358
FRIOR APPLICATION NUMBER: US 60/166,358
FRIOR APPLICATION NUMBER: US 60/166,358
FRIOR APPLICATION NUMBER: US 60/166,358
FRIOR APPLICATION NUMBER: US 60/166,358
FRIOR PILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-08-09
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Sequence 322491, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
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, OTHER INFORMATION: n = A,T,C or G
US-10-027-632-322491
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Best Local Similarity 90.7
Matches 411; Conservative
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LENGTH: 570
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                                                                                    APPLICANT: WIGNALIDES:
APPLICANT: WIGNALIDES:
APPLICANT: WIGNALIDES:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/157,363
PRIOR APPLICATION NUMBER: US 60/157,363
PRIOR APPLICATION NUMBER: US 60/157,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
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Pred. No. 3e-105;
2; Mismatches 39; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 322492
LENGTH: 570
Sequence 322492, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (1)...(570)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-322492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 25.5%;
Best Local Similarity 90.7%;
Matches 411; Conservative
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361
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23.8%; Score 353; DB 13; Length 551;
Best Local Similarity 92.0%; Pred. No. 1.3e-97;
Matches 412; Conservative 2; Mismatches 30; Indels
PRIOR FILING DATE: 2000-07-12
PRIOR PAPPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1000-02-24
PRIOR FILING DATE: 1999-1-23
PRIOR FILING DATE: 1999-04-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SOCTWARE: PSELSEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 322574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature

| LOCATION: (1)...(551)

| OTHER INFORMATION: n = A,T,C or G

US-10-027-632-322574
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                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Human
FEATURE:
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                                              Sequence 4312, Application US/10029386
Sequence 4312, Application US/10029386
Sequence 4312, Application Vo. US20030194704A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR (TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXPERESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE REFERENCE: AEDMICA-X-2
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 4312
LENGTH: 521
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
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OTHER INFORMATION: MAP TO ACO21619.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.81
OTHER INFORMATION: EST HUMAN HIT: BE734284.1, EVALUE 0.00e+00
OTHER INFORMATION: SNISSPROT HIT: P10269, EVALUE 4.00e-26
OTHER INFORMATION: NI HIT: AF208161.1, EVALUE 0.00e+00
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24.6%; Score 364; DB 16; Length 521;
Best Local Similarity 91.7%; Pred. No. 5.2e-101;
Matches 385; Conservative 0; Mismatches 35; Indels
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                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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                  RESULT 26
US-10-029-386-4312/c
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US-10-029-386-4312
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Score 353; DB 17;
Pred. No. 1.3e-97;
2; Mismatches 30;
              PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-02-24
PRIOR PRILING DATE: 1999-11-23
PRIOR PRILING DATE: 1999-11-23
PRIOR PRILING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
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PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PSESEQ FOR WINDOWS VERSION 4.0
SOFTWARE: 551
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; OTHER INFORMATION: n = A,T,C
US-10-027-632-322574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 23.8%;
Best Local Similarity 92.0%;
Matches 412; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Delymorphisms in the Human Genome FILE REFERENCE: 108827.128 CURRENT APPLICATION NUMBER: US/10/027,632
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Pred. No. 1.3e-97;
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                  PRIOR PELING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PELING DATE: 2000-04-20
PRIOR PELING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR PELING DATE: 2000-03-29
PRIOR PLILING DATE: 2000-02-24
PRIOR PLILING DATE: 2000-02-24
PRIOR PLILING DATE: 1999-11-23
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-28
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PRIOR PELING DATE: 1999-09-09
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Best Local Similarity 92.0%;
Matches 412; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1). .. (551)
COTHER INFORMATION: n
US-10-027-632-322575
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Length 551;

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281 ACCTTCACTGCCCACACCCATATGCCCCACAAATGCTGTAACTCTGCCACTCTTTGCATG 340
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                                                                                                                                                                                                                                                                                                                                                          ACCITCACTGCCCACACACCCATATGCCCCGCAACTGCTATAACTCTGCCACTCTTTGCATG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCACCCCCTCCATGCTGCTGTACAACCAGTAGCTCCCCTTACCAAGAGTTTCTATGAAGA 120
                                                                                                                                                                                                                                                       121 ACGCGCCTTCCTGGAAATATTGATGCCCCATCATATAGGAGTTTATCTAAGGGAAACTCC
                                                                                                                                                                               162 GCACCCGCTCCATGCCGCTGTACGACCAGTAGCTCCCCTTACCAATAGTTTCTATGRAGA
                                                                                                                                                                                                                                                                                  222 AIGCGGCTTCCTGGAAATATTGATGCCCCATCAWATAGGAGTTTATCTAAGGAAAC-CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATGCAAATACTCATTATTGGACAGGAAAATGATTAATCCTAGTTGTCCTGGAGGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 322575, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION:
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
  4
30; Indels
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APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REPERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US/017,161
PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 1393
LENGTH: 822900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOCATION: (74625). (74724)
OTHER INFORMATION: a, t, c, g, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAWE/KEY: modified base
LOCATION: (85854). (85953)
OTHER INFORMATION: a, t, c, g, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KET: modified base
LOCATION: (17785). (17884)
OTHER INFORMATION: a, t, c, g, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g, unknown or other
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NAME/KEY: modified_base
LOCATION: (4966)..(4966)
OTHER INFORMATION: a, t, c, g, unknown
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NAME/KEY: modified_base
LOCATION: (61159)..(61258)
OTHER INFORMATION: a, t, c,
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(273663)..(273702)
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(482589)..(482596)
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(822485)..(822700)
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LOCATION: (67605)...(67704)
OTHER INFORMATION: a, t, c,
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(140545)..(140693)
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(261786)..(261845)
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LOCATION: (4848)..(4947)
OTHER INFORMATION: a, t, c,
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LOCATION: (1)..(822900)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
(201)..(1068)
                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                  FEATURE:
LOCATION: source
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LOCATION:
FEATURE:
NAME/KEY: n
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LOCATION:
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NAME/KEY:
LOCATION:
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LOCATION:
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FION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 AIGCGGGCTTCCTGGAAATATTGAIGCCCCATCAWATAGGAGTTTATCTAAGGAAAC-CC 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCTTCACTGCCCACACCCCATATGCCCCGCAACTGCTATAACTCTGCCACTCTTTGCATG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAGCCACTGTCTGTTGGACTT-ACTTCACCCATACCAGTATGTCTGATGGGGGTGGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 23.8%; Score 353; DB 17; Length 551; Best Local Similarity 92.0%; Pred. No. 1.3e-97; Matches 412; Conservative 2; Mismatches 30; Indels
    CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR PELING DATE: 2002-04-30
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-4
PRIOR FILING DATE: 2000-02-4
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-3
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FABLESEQ FOR WINDOWN VERSION 4.0
SERIOTH: 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAGCACCCCTAGCCCCTACAAAGGACTA 447
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US-10-292-798-1393/C
US-10-292-798-1393/C
SQUUENCE 1393, Application US/10292798
SPUBLICALION NO. US20030238833A1
GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1)...(551)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-322575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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NAME/KEY: modified_base

us-09-319-156b-9.rnpb

FEATONE: Modified base
LOCATION: (724960)...(725059)
OTHER INFORMATION: a, t, c, g, unknown or other EAND.KEY: modified base OCATION: (370279)...(370279) THER INFORMATION: a, t, c, g, unknown or other PAINTEN MODIFIED DASE
LOCATION: (370285)...(370287)

THER INFORMATION: a, t, c, g, unknown or other TAME/KEY: modified base OCATION: (370289) ... (370291) OTHER INFORMATION: a, t, c, g, unknown or other NAWE/KEY: modified base LOCATION: (409961)..(410060) OTHER INFORMATION: a, t, c, g, unknown or other NAWE/KEY: modified base LOCATION: (367588) ...(367588) OTHER INFORMATION: a, t, c, g, unknown or other NAME/KEY: modified base LOCATION: (367595)...(367595) OTHER INFORMATION: a, t, c, g, unknown or other NEW KEY: modified base LOCATION: (367613) ... (367614) OTHER INFORMATION: a, t, c, g, unknown or other LOCATION: (367985)...(367985) OTHER INFORMATION: a, t, c, g, unknown or other NAME, KEY: modified base LOCATION: (367993) ... (367993) OTHER INFORMATION: a, t, c, g, unknown or other ION: (367998)...(367998) INFORMATION: a, t, c, g, unknown or other NAME/KEY: modified base OCATION: (370273) ... (370277) OTHER INFORMATION: a, t, c, g, unknown or other NAME/KEY: modified base LOCATION: (370281) .. (370282) OTHER INFORMATION: a, t, c, g, unknown or other LOCATION: (385643) ... (385742) OTHER INFORMATION: a, t, c, g, unknown or other or other unknown or other LOCATION: (367573)..(367573) OTHER INFORMATION: a, t, c, g, unknown or other LOCATION: (367995)...(367996) OTHER INFORMATION: a, t, c, g, unknown or LOCATION: (410096)...(410096) OTHER INFORMATION: a, t, c, g, unknown LOCATION: (417384)...(417483) OTHER INFORMATION: a, t, c, g, NAME/KEY: modified_base LOCATION: (726106)..(726205) NAME/KEY: modified base NAME/KEY: modified_base NAME/KEY: modified_base NAME/KEY: modified_base NAME/KEY: modified_base NAME/KEY: modified_base

56961 GATGCCTAAATGGCACTCTGAAAGAACAATGCTTTCTCCCTTTCTAGCACCTCCCATGT 56902 56841 cccrratrorcccritriatriciaecadroccaaractececadecrecerrecaarie 56782 56901 CCATATATACTGAACAGGAGTTACAAAGTCTCCTTATACCCCCAATCTCGCCACGCGGG , 953 TACCCATTCTTTCTTATCAGAGCAGGAGTGCTAGGCAGACTAGGTACTGGCATTG 773 CCACACGAATAGICIGCCIACCCICAGGAATATITITIGICIGIGGIACCICAGCCIAIC 833 ATTGTTTGAATGGCTCTTCAGAATCTATGTGCTTCCTCTCATTCTTAGTGCCCCCTATGA 893 CCATCTACACTGAACAAGATTTATACAATCATGTCGTACCTAAGCCCCCACAAAAAAGAG Gaps 21.5%; Score 318.6; DB 17; Length 822900; 68.5%; Pred. No. 3.2e-85; ive 0; Mismatches 214; Indels 9; G unknown or other NAME/KEY: modified base LOCATION: (744360)...(744459) OTHER INFORMATION: a, t, c, g, unknown or other NAME/KEY: modified base LOCATION: (734441)...(734441) OTHER INFORMATION: a, t, c, g, unknown or other LOCATION: (748430)...(748529) OTHER INFORMATION: a, t, c, g, unknown or other NAME/KEY: modified base LOCATION: (730296)...(730395) OTHER INFORMATION: a, t, c, g, unknown or other OTHER INFORMATION: a, t, c, g, unknown or other LOCATION: (728849)...(728948) OTHER INFORMATION: a, t, c, g, unknown or other unknown or other unknown or other unknown or other unknown or AAME/KET: modified base COCATION: (731863)..(731962) DTHER INFORMATION: a, t, c, g, unknown NAME/KEY: modified base LOCATION: (734124)...(734223) OTHER INFORMATION: a, t, c, g, NAME KEY: modified base LOCATION: (738576)..(738675) OTHER INFORMATION: a, t, c, g, NAME/KEY: modified base LOCATION: (740924)..(741023) OTHER INFORMATION: a, t, c, g, NAME/KEY: modified base LOCATION: (735752)..(735851) OTHER INFORMATION: a, t, c, g, 6 FEATURE:
NAME/KEY: modified base
LOCATION: (727470).. (727569)
OTHER INFORMATION: a, t, c, NAME/KEY: modified base LOCATION: (754323)...(754422) Query Match
Best Local Similarity 68.55
Matches 486; Conservative FEATURE: NAME/KEY: modified base FEATURE: NAME/KEY: modified_base δ g ò g ò ઠે

56962

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APPLICANT: FLANCE

BESEME, FRELL.

BESEME, FRELL.

BESEME, FRELL.

BESEME, FRELL.

BESEME, FRELL.

BERNANGOS BACCALA, GLAUCIA

KOMURIAN-PRADEL, FLORENCE

JOLIVET-REYNAUD, COLETTE

MANDRAND, BERNARD

GARSON, JERENY

TUKE, PHILIP

TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS

THERAPEUTIC PURPOSES

THERAPEUTIC PURPOSES
                                                                                                                                                                                        1199
                                                                                                                                                                                                                                                                                                                                              1319
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                                                                                                                                                                                                                                                                 1200 AGGAGAAGGAACGCTGTTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGA 1259
                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                  180
                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 TITACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAAT 300
                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                              1260 AATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAAAACACCGAACGCTGGGGCCT
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                                                                                                                                                                                                                                                                                                       61 AGGGGAAGAATGCTGTTAGTTATGTTAATCTAGAATCATTACTGAGAAAGTTAAAGA
                                                                                                                                                                                      1140 TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTT
                                                                                                                                                                                                                            Gaps
                                                                                                                                                 ö
                                                                                                           Length 1329;
                                                                                                                                                 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1440 TGAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAACCCCA 1481
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                                                                                                           Score 302; DB 8;
Pred. No. 1.1e-81;
0; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/114,104
FILING DATE: 03-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDIA
ODERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,847
FILING DATE: 26-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 108, Application US/10114104 Publication No. US20030198647A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERE
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION
                                                                                                               20.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
                                                                                                             Query Match
Best Local Similarity 92.7
Matches 317; Conservative
TYPE: nucleic acid
STRANDEDNESS: single
      ; TYPE: nucleic acid
; STRANDEDNESS: sinc
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-979-847-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-114-104-108
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APPLICANT: BERNOW, HERVE
APPLICANT: BERNOW, HERVE
APPLICANT: BEDIN, FREDERIC
APPLICANT: BARNINGS-BACCIA, GLAUCIA
APPLICANT: PARANHAN-PRADEL, FLORENCE
APPLICANT: VOMURIAN-PRADEL, FLORENCE
APPLICANT: MANDRAND, BERNARD
APPLICANT: MANDRAND, BERNARD
APPLICANT: MANDRAND, BERNARD
APPLICANT: TUKE, PHILIP
TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
TITLE OF INVENTION: THERAPEUTIC PURPOSES
NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 56370
                                        56664
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                                                                                                             56663 TAGTCCTTCAAAACCGGAGAGCCCTAGACTTATTAACAGCTAAAAAAAGGAGGAACTTGC 56604
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                          TGGAACAGGTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAG
                                                                               1133 TAGTCCTTCAAAATCGAAGAGCTTTAGACTTGCTAAACGCGCAAAAGAGGGGGAACCTGTT
                                                                                                                                                          1193 TATTITIAGGAGAAGAACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAG
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ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,847
FILING DATE: 26-NOV-1997
CLASSIFICATION NUMBER: US/08/979,847
FILING DATE: 26-NOV-1997
CLASSIFICATION NUMBER: WPB 39046A
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INPORMATION:
TRISPHONE: 70-916-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 108, Application US/08979847
Publication No. US20030039664A1
GENERAL INFORMATION:
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TELEFAX: 703-836-62787
INFORMATION FOR SEQ ID NO: 5EQUENCE CHARACTERISTICS:
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US-08-979-847-108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: MAP TO AL022067.1

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.95

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BOULT LIVER, SIGNAL = 7.1

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 7.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR FILING DATE: 2001-01-30
PRIOR PTLING DATE: 2001-01-30
PRIOR PTLING DATE: 2001-01-30
PRIOR PTLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2001-01-39
PRIOR PILING DATE: 2001-01-39
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PRIOR PILING DATE: 2001-01-39
PRIOR PILING DATE: 2001-01-39
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ORGANISM: Homo sapiens
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; Sequence 14030, Application US/09864761
; Patent No. USZO020048763A1
; GENERAL INFORMATION:
; APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David R.
; APPLICANT: Hanzel, David R.
; APPLICANT: Hanzel, David R.
; APPLICANT: Chen, Wenbheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: HUMBER EXPRESSION ANALYSIS BY MICROARRAY
; FILE REPRENCE: Accomica-X-1
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-30
; PRIOR FILING DATE: 2000-02-26
; PRIOR FILING DATE: 2000-03-26
; PRIOR FILING DATE: 2000-08-03
; PRIOR FILING DATE: 2000-09-27
; PRIOR FILING DATE: 2000-09-27
; PRIOR FILING DATE: 2000-09-27
; PRIOR FILING DATE: 2000-09-27
; PRIOR FILING DATE: 2000-09-27
; PRIOR FILING DATE: 2000-09-30
; PRIOR FILING DATE: 2000-09-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
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                   NAME: BERRIDGE, WILLIAM P.
REGISTRATION WUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
TELEPAN: 703-836-6400
TELEPAN: 703-836-6400
TELEFAX: 703-836-5787
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGHY: 1329 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-10-114-104-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 92.77
Matches 317; Conservative
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COCATION: (1)...(625)
COTHER INFORMATION: n = A,T,C or G
US-10-027-632-316412
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NAME/KEY: misc_feature
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US-10-027-632-86541/c
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      377
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                                                                                                                                                                                                                 APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
FRIOR PILING DATE: 2000-07-12
FRIOR PILING DATE: 2000-04-20
FRIOR PILING DATE: 2000-04-20
FRIOR PILING DATE: 2000-04-20
FRIOR PILING DATE: 2000-04-20
FRIOR PILING DATE: 2000-03-29
FRIOR PILING DATE: 2000-02-24
FRIOR PILING DATE: 1999-11-23
FRIOR PILING DATE: 1999-11-23
FRIOR PILING DATE: 1999-09-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                         Sequence 316412, Application US/10027632 Publication No. US20020198371A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           // LOCATION: (1)...(625)
// OTHER INFORMATION: n = A,T,C or G
US-10-027-632-316412
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                                                                                      RESULT 35
US-10-027-632-316412/c
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US-10-027-632-316412/c
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LENGTH: 625
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1) Sequence 86541, Application US/10027632

1) Publication No. US20020198371A1

1) GENERAL INFORMATION:
1) APPLICANT WANG, David G.
1) TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
1) TITLE OF INVENTION: Polymorphisms in the Human Genome
1) TITLE OF INVENTION: Polymorphisms in the Human Genome
1) TITLE OF INVENTION: 2002-04-30
1) CURRENT APPLICATION NUMBER: US/10/027,632
1) CURRENT APPLICATION NUMBER: US 60/198,676
1) PRIOR APPLICATION NUMBER: US 60/198,676
1) PRIOR APPLICATION NUMBER: US 60/193,483
1) PRIOR FILING DATE: 2000-04-20
1) PRIOR FILING DATE: 2000-03-29
1) PRIOR APPLICATION NUMBER: US 60/193,483
1) PRIOR APPLICATION NUMBER: US 60/193,483
1) PRIOR APPLICATION NUMBER: US 60/193,483
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TITLE REFERENCE: 108927.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
NUMBER OF SQ ID NOS: 325720
SUGTWARRE: FRAESQ FOR WINDOWS VERSION 4.0
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US-09-664-761-7501, Application US/09864761

Jeatent No. US202004873A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

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APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Menheng BERRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Acomica.X-1

CURRENT PRILING DATE: 2001-05-20

PRIOR PRILING DATE: 2001-05-20

PRIOR PAPLICATION NUMBER: US 60/180,312

PRIOR PLING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PLING DATE: 2000-02-04

PRIOR PLING DATE: 2000-03-07

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

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Best Local Similarity 86.3%; Pred. No. 1.5e-59;
Matches 253; Conservative 0; Mismatches 40
                                                                                                                      ; LOCATION: (1)...(619); OTHER INFORMATION: n = A,T,C or G
US-10-027-632-86541
                                                                                               NAME/KEY: misc_feature
                                          ORGANISM: Human
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 10827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/128,006
PRIOR APPLICATION NUMBER: US 60/128,006
PRIOR FILING DATE: 2000-07-12
PRIOR PELLING DATE: 2000-07-20
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/198,518
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-09-38
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-10-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PASTESQ for Windows Version 4.0
SENGTH: 619
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                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(619)
OTHER INFORMATION: n = A,T,C or G
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US-10-027-632-86541/c
                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-027-632-86541
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1226 ATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAAATTCGAGATCGAATACAATGTAGAG 1285
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CTHER INFORMATION: MAP TO AP001697.1

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.3

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.91

OTHER INFORMATION: WITH: AF208161.1, EVALUE 1.008-108

OTHER INFORMATION: SYPRESSED IN HELA, SIGNAL = 0.91

OTHER INFORMATION: SYPRESSED IN HELA, SIGNAL = 0.091

OTHER INFORMATION: SYPRESSED IN HELA, SIGNAL = 0.091

OTHER INFORMATION: SYPRESSED IN HELA, SYALUE 1.008-108

US-10-029-386-20259
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 14.4%; Score 213; DB 16; Length 494; Best Local Similarity 85.6%; Pred. No. 1.7e-54; Matches 261; Conservative 0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 completed: February 21, 2005, 19:18:14
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Publication No. US20030194704A1
GENERAL INFORMATION:
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Pred. No. 2e-56;
0; Mismatches 21; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WE EXPRESSED IN PLACENTA, SIGNAL = 2.5
WE EXPRESSED IN HERA, SIGNAL = 3.9
WE EXPRESSED IN HEART, SIGNAL = 2
WE EXPRESSED IN PETAL LIVER, SIGNAL = 3.3
WE EXPRESSED IN BONE MARROW, SIGNAL = 3.2
WE EXPRESSED IN LUNG, SIGNAL = 1.9
WE EXPRESSED IN BOULT LIVER, SIGNAL = 1.9
WE EXPRESSED IN BRAIN, SIGNAL = 2.2
   PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PILING DATE: 2000-01-30
PRIOR FILING DATE: 2000-09-31
PRIOR FILING DATE: 2000-09-31
PRIOR FILING DATE: 2000-09-31
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 7501
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Best Local Similarity 91.7
Matches 232; Conservative
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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LK622175
full-length cDNA clone CS0DI051YM13 of Placenta Cot 25-normalized of Homo sapiens (human).
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1 (bases 1 to 2500)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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BX388917
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BX368759
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                                                                                         CR735592
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BX326300 1
BX337769 1
BX378303 1
BX429316 1
BX388917 1
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                                          BE019603
BG572445
BX450495
CR735592
BX365066
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BX409035
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Placenta
/plasmid="pCMVSPORT_6"
BX430050
BX409304
BX409304
BES104603
BES104603
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BX55645
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Homo sapiens (human)
Eukann
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93.8%;
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Best Local Similarity
Matches 1389; Conserv
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389.8
373.2
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537.6
536.4
535.2
478.6
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421.6
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Genoscope.

Direct Submission

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage:

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage:

BP 191 91006 BVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

1nt strand cDNA was digested with Not I and cloned

into the Not I and EcoR v sites of the pcMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen.
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                                                                         1261 ATTCGAGATCGAATACAATGTAGAGCAGAGCTTCAAAACACCGAACGCTGGGGCCTC
                                                                                        Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
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| organism="Homo sapiens"
| mol_type="mRNA"
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| clone="CSODIO51YM13" |
| clone="type="PLACENTA COT 25-NORMALIZED" |
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2 rue Gaston Cremieux, CP 5706 - 91057 BVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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935 bp mRNA linear EST 29-APR-2004
BX391741 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODI051YM13 3-PRIME, mRNA sequence.
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Full-length cDNA libraries and normalization
Unpublished (2001)
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  GGAGAAGAACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAA
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Contact: Genoscope
Genoscope - Centrar National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequenceScope.cns.fr, Web: www.genoscope.cns.fr
Email: sequenceScope.cns.fr, Web: www.genoscope.cns.fr
1st strand CDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                     For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAE023ZF07_AE02167_1&c=4215.r
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/tissue type="PlACENTA" COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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Pred. No. 2e-229;
0; Mismatches 56;
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
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larity 93.7%;
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BX347952 GI:30375235
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 955)
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                                                                                              ACTGACCCGGGGACATAGCACCCCTAGCACAAAGGACTAGTTCTCTCAAAACTACA
                                             TGATGGGGGTGGAATTCAAGGTCAGGCAAGAGAAAAACAAGTAAAGGAAGCAATCTCCCA
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CACCCATACCAGTATGTGTGATGGGGGTGGAATTCAAGGTCAGGCAAGAGAAAACAAGT
                                                                            AAAGGAAGCAATCTCCCAACTGACCCGGGGACATAGCACCCCTAGCCCCTACAAAGGACT
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/ Organism="Homo sapiens"

/ Organism="Homo sapiens"

/ Ab I Ltpe="mRNA"

/ Clone="CSOD1051XM13"

/ Clone="Ib" type="PLACENTA COT 25-NORMALIZED"

/ Clone="lb" strand CDNA was primed with a NotI-oligo(dT)

/ note="lst strand CDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand CDNA was primer. Managested with Not I and cloned into the Not I and Econ V sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Genoscope
Genoscope - Centre National de Sequencage
Z rue Gastono Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
E rue Gastono Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Estail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVEPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAF0272B05_AF02531_1&C=4215.r
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BX389656 BX389656. GI:30462930
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                                                                                                                           AAAAGAGTACCCATTCTTTTGTTATCAGAGCAGGAGTGCTAGGCAGACTAGGTACT 1005
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Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 931)
Liv.B., Gruber, C., Jessee, J. and Polayes, D.
Full.length cDNA libraries and normalization
Unpublished (2001)
                                                                                      GCCTATCATTGTTTGAATGGCTCTTCAGAATCTATGTGCTTCCTCTCATTCTTAGTGCCC
                                 CCTATGACCATCTACACTGAACAAGATTTATACAATCATGTCGTACCTAAGCCCCACAAC
                                                                                                                                           GGCATTGGCGGTATCACAACCTCTACTACTACTACAAACTATCTAAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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AUTHORS
TITLE
JOURNAL
COMMENT
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BX389656
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154

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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotL-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned
the Not I and BCORV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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1 (bases 1 to 903)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                  TAGTGCCCCCTATGACCATCTACACTGAACAAGATTTATACAATCATGTCGTACCTAAGC 937
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GTACCTCAGCCTATCATTGTTTGAATGGCTCTTCAGAATCTATGTGCTTCCTCTCATTCT
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Contact: Genoscope
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For more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTCCCTAGCAGCAGTAGTCCTTCAAAATCGAAGA 1152
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/db_xref="taxon:9606"
/clone="CS0DE013YI20"
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//organism="Homo sapiens"
//mol_type="mRNA"
//mol_type="mRNA"
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//orde="list strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime and enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime-
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 872)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraties and normalization

Unpublished (2001)
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Pred. No. 9.7e-210;
0; Mismatches 64;
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Matches 808; Conservative (
        sapiens (human)
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                   /tissue type="PLACENTA"
/close lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and BCORV sites of the pCMVSPORT 6 vector.
Library was not normalized."
                                                                                                                                                                                                                 This sequence belongs to sequence cluster 4215.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOBAA008ZE02_CS00686_1&c=4215.r
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       Eukaryota, Metazoa, Chordata, Craniata, Verte
Mammalia, Eutheria, Primates, Catarrhini, Hon
1 (bases 1 to 883)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Tall-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE012YJ24"
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Matches 825;
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BX388766 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODIO44YKO6 3-PRIME, mRNA sequence.
BX388766. GI:46877917
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequef@genoscope.cns.fr. Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSFORT & vector Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAD009ZB06_AD00811_i&c=4215.r
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1. (bases 1 to 877)

1. M.B., Gruber, C., Jessee, J. and Polayes, D.

Full.length cDNA libraries and normalization

Unpublished (2001)
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                                            TCCCCCTGCACTTCAGGCCATACATTCCTGTTCCTGAACAATGGAACAACTTCA
                                                                  GCACAGAAATAAACACCACTTCCGTTTTAGTAGGACCTCTTGTTTCCAATCTGGAAATAA
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Pred. No. 3.7e-204;
0; Mismatches 55;
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Matches 803; Conservative
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
/inche="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(T) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             division of Invitrogen.
This sequence belongs to sequence cluster 4215.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOBAA008ZE02_CSO0686_2&c=4215.r
                                                                                                                                                                                                                  1283
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BX408734 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE012XJ24
5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                  116
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 921)
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                                                                                                                                                         235 GCTAACCGCTGAAAGAGGGGGGAACCTGTTTAATTTTTAGGGGAAGAATGCTGTTATTATGT
                                                                                                                                                                                                                         TAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAAATTCGAGATCGAATACAATGTAG
                                                                                                                                                                                                                                                                               175 TAATCAATCCGGAATCGTCACTGAGAAAGTTAAAGAAATTCGAGATCGAATACAACGTAG
                                                                                                                                                                                                                                                                                                                                            1284 AGCAGAGGAGCTTCAAAACACCGAACGCTGGGGCCTCCTCAGCCAATGGATGCCCTGGGT
                                                                                                                                                                                                                                                                                                                                                                               GCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTAGGAGAAGAACGCTGTTATTATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTCCCCTTCTTAGGACCTCTAGCAGCTCTAATATTGTTACTCCTCTTTGGACC 1397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 709.8; DB 5;
Pred. No. 1.2e-198;
0; Mismatches 98;
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/db_xref="taxon:9606"
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Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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[2 [1 (w.B., Gruber, C., Jessee, J. and Polayes, D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOAU012ZB04_U01082_1&c=4215.r. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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llarity 92.6%; Pred. No. 6.8e-200;
Conservative 0; Mismatches 60;
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AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D. TITLE Full-length cDNA libraries and normalization JOURNAL Unpublished (2001) COMMENT Genoscope Contact: Genoscope 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr 1st strand cDNA was primed with a NoII-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with NoI I and cloned into the NoI I and EcoR V sites of the pCMNSORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7108.r FOR more information about this cluster, see http://www.genoscope.cns.fr/cdna?e=CSOAU010ZB08_U0922_1&c=7108.r. FEATURES 1. Add	/db_xref="text"/clone="CS001"/clone="Lb="ref"/clone="lb="ref"/	atches 58; Indels 2; Gaps GAGGTCTCAGCCCAAA-CCCTACTAACTGTTG	Qy 620 ACAACTTCGGCACAGAATAAACACCACTTTCGTTTTAGTAGGACCTCTTGTTTCCAATC 679 Db 717 CAACTTTCGGCACAGAATAAACCCACTTCGTTTTTTTTTT	Oy 860 TGTGCTTCCTCTTTTTGGCCCCTATGACCATCTACACAGATTTATACA 919 477 TGTGCTTCCTCTTTTTTGTGCCCCCTATGACCATCTACACAGATTTATACA 418 Oy 920 ATCATGTGGTACCTAAGCCCCCAACAAGAGGTACCCATTCTTCTTTTTTTATACA 418 Db 417 GTTATGTCATATCTAAGCCCCGCAACAAAAGAGTACCCATTCTTCTTTTTTTATAGGG 979 Oy 980 CAGAGTGCTAAGCTAGGTACTGGCATTGGCAGTTCTTCCTTTTTTTT
		CTTCA CTTCA CTTCA AATAA AATAA CTCCC		SULT 15 347111/c S147111/c S147111 Homo sapiens PLA CLOSS EST. STAT111 Homo sapiens PLA CLOSS EST. STAT111 GI:30375145 STAT111 GI:30375145 STAT111.1 GI:30375145 STAT1111.1 GI:30375145 STAT11111.1

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On May 8, 2003 this sequence version replaced gi:30447710.
Contact: Genoscope
Contact: Genoscope
Centes National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EWRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
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was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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BX368078 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
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1. (bases 1 to 846)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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                                           CIGGAGGACTIGGAGCCACTGICTGTTGGACTTACTTCACCCATACCAGTATGTCTGATG
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
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into the NotI and EcoR V sites of the pCMVSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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1 (bases 1 to 828)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.'
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    PITTCTTGGAGAATGCAGCGTCCCGG-AATATTGATGCCCCATCGTATAGGAGTCTTTCTA

                                 CCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTTCAAAATCGAAGAGCTTTAG
                                                                                                                   CCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTTCAAAATCGAAGAGCTTTAG
                                                                                        1160 ACTIGCTAACCGCCAAAAGAGGGGGAACCIGTTTATTTTAGGAGAAGAACGCTGTTATT
                                                                                                                                                                     1220 ATGTTAATCCAGAATTGTCACTGAGAAAGTTAAAGAAATTCGAGATCGAATACAAT
                                                                                                                                                                                                            Argitaaticaaticgaaticgicactgagaagitaaagaaattcgagatcgaatacaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCTATGAAGAACGCGGCTTCCTGGAAATATTGATGCCCCCATCATATAGGAGTTTAATCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                 GTAGAGCAGAGGAGCTTCAAAACACCGAACGCTGGGGCCTCC 1321
                                                                                                                                                                                                                                                                                      GTAGAGCAGAGCTTCGAAACACTGGACCTGGGGCCGCCC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 703.2; DB 5;
Pred. No. 1.1e-196;
0; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BX367907
BX367907.1 GI:30459586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.5%;
llarity 93.8%;
Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Genoscope
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Matches 754; (
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              1100
                                                                                                                                                                                                                                                   1280
                                                     237
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AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                  RESULT 16
BX367907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
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On May 2003 this sequence version replaced gi:30462931.
Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
I rue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAF027ZB05_AF02531_2&c=4215.r
                                                                                                                                                                                                BX389657 BX 29-APR-2004 BX389657 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI051YM13 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             raaaagaagraarcreecaacreacecgggracarggcaccrerageccraaaagaac 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="CSODIO51YM13"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 TAGATCTCTGAAAACTACATGAAACCTCCGTACCCATACTCGCCTGGTAAGCCTATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 326 TCACCCATACCAGTATGTCTGATGGGGGTGGAATTCAAGGTCAGGCAAGAGAAAAACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         446 TAGITCICICADADACTACAIGADACCCTCGGIACCCATACTCGCCTGGIGAGCCTATITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          386 TAAAGGAAGCAATCTCCCAACTGACCCGGGGACATAGCACCCCTAGCCACCTACAAAGGAC
Gaps
                                                                                                                                                                                                                                                                                                                                                                         Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 995;
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                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Primates; Catarrhini; Hor
1 (bases 1 to 995)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Li,M.B., Gruber,C., Jessee,J. and Polayes,D.
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 696.2; DB 5;
Pred. No. 1.4e-194;
0; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                  BX389657.2 GI:46875146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.0%;
                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
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                                                                              1303 ACCGAAC 1309
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Best Local Si
Matches 826
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KEYWORDS
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ORGANISM
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                                                                                                                                                                                                                            DEFINITION
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AUTHORS
TITLE
JOURNAL
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                                                                                                                                                                     RESULT 18
BX389657
                                                                                                                                                                                                                                                             ACCESSION
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                                                                                 1. :846
// Organism="Homo sapiens"
// nol_type="mNAN"
// db_xref="taxon:9606"
// clone="CSODIO51YM13"
// clone="CSODIO51YM13"
// clone="Los type="Flacenya COT 25-NORMALIZED"
// clone="lst strand cDNa was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNa was primed with not I and aloned into the Not I and EcoR V gites of the pCMVSPORT 6 vector. Library was normalized."
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                          For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOAU012ZDO5_U01092_1&c=4215.r. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1003 ACTGGCATTGGCAGTATCACAACCTCTACTACTACTACAAACTATCTCAAGAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1063 AATGGTGACATGGAACAGGTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCC
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                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          526 CATGAGGTCTCAGCCC-AAAACCCTACTAACTGTTGGATGTGCCTCCCCCTGCACTTCA-
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                                                                                                                                                                                                                                                                                                                            Length 846;
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                56;
                                                                                                                                                                                                                                                                                                                          Score 698.6; DB 5;
Pred. No. 2.5e-195;
                                                                                                                                                                                                                                                                                                                                                                Mismatches
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0
                                                                                                                                                                                                                                                                                                                          47.2%;
92.8%;
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Les 786; Conserv
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                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                        FEATURES
                                                                                                                                                                                                                                                                                           ORIGIN
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1. .924
/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="C$ODIO44YK06"
/clone="C$ODIO44YK06"
/clone="Lype="PLACENTA COT 25-NORMALIZED"
/clone Tib="Homo sapiens PLACENTA COT 23-NORMALIZED"
/clone Tib="Homo sapiens PLACENTA COT 20-NORMALIZED"
/clone Tib="Homo sapiens PLACENTA COT 20-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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                                  For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAA016ZH06_CS01489_1&c=4215.
to sequence cluster
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr. Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVBPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
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BX347314 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA CLONE SCODIO44YK06 5-PRIME, mRNA sequence.

BX347314
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1. (bases 1 to 924)
11, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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171 120 231 180 291 240 351 300 411

Fri

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Vencer, J.C.

Vencer, J.C.

Use a random human BAC End Sequence Database for Sequence-Ready
Map Building
In Unpublished (1998)
Other_GSSs: CITB1-E1-2506C15.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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                                                                                                            GTGCTAGGCAGACTAGGTACTGGCATTTGGCAGTATCACAACCTCTACTACTACTAC 1044
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Adams, D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                   662
                                                                                                                                                                                                                                                                                    363 GTCATATCTAAGCCCCGCAACAAAAGAGTACCCATTCTTCCTTTGTTATAGGAGCAGGA 422
303 ITCCTCTCTTATAGTGCCCCCTATGACCATCTACACTGACAAGATTTATACAGTTAT 362
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/clone lib="CITBL-B1"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
Calrech Human BAC Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                            663 AATCAATCCGGGATCGTCACTGGAGAAGTTAAAGAAATTCGAGATCGAATACAACGT 720
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/db_xref="taxon:9606"
/clone="2506C15"
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Venter, J.C.
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         831 AGCCATACTACATACACAAACCAAAATTCCCATGCATCAAGGTGGTAACTCCTCCCACACA 889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 81-438-52-3975
Fax: 81-438-52-3986
Fax: 81-438-52-3986
Faxi 81-438-52-3986
Fazil: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                          Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Halix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.7%; Score 647; DB 1; I 94.6%; Pred. No. 4.9e-180; iive 0; Mismatches 38;
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/db_xref="taxon:9606"
/clone="placElo08489"
/tissue_type="placenta"
/clone_lib="placenta"
/note="Vector: pMEI8SFL3"
                                                 781 ATAGICIGCCIACCCICAGGAAIATITI 809
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/organism="Homo sapiens"
                                                                    AU138405.1 GI:10999926
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Homo sapiens
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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

Location/Qualifiers
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                                                                                                                                                                                                                   Score 628.6; DB 1;
Pred. No. 1.4e-174;
0; Mismatches 37;
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/organism="Homo sapiens"
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/db xref="taxon:9606"
/clone="PLACE1007839"
/clone lib="PLACE1"
/clone lib="PLACE1"
/note="Vector: pME18SFL3"
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larity 94.6%;
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Matches 660;
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                                                                                                                              61 CAAAGGACTAGTTCTCTCTAAACTACATGAAACCCTCCGTACCCATACTCGCCTGGTGAG 120
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 702)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                       181 TTGGATGTGCCCCCCTGCACTTCAGGCCATACATTTCAATCCCTGTTCCTGAACAATG
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                                                                                                                                                                                                                                                                                              241 GAACAACTTCAGCACAGAAATAAACACCCACTTCCGTTTTAGTAGGACCTCTTGTTTCCAA
                                                                                                                                                                                                                                                                                                                                                     301 TCTGGAAATAACCCATACCTCAAACTCACCTGTGTAAAATTTAGCAATACTATAGACAC
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                                                                          1 AAAACAAGTAAAGGAAGCAATCTCCCAACTGACCCGGGGACATAGCACCCCTAGCCCCTA
                                                                                                      CAAAGGACTAGTTCTCTCAAAACTACATGAAACCCTCCGTACCCATACTCGCTGGTGAG
                                                                                                                                                               CCTATTTAATACCACCCTCACTCGGCTCCATGAGGTCTCAGCCCAAAACCCTACTAACTG
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                                              AAAACAAGTAAAGGAAGCAATCTCCCAACTGACCCGGGGACATAGCACCC
                    Indels
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HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
    7.8e-175;
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     Pred. No. 7.8e
0; Mismatches
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Stausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CCTGTTCCTGAACAATGGAACAACTTCAGCACAGAAATAAACACCACTTCCGTTTTAGTA
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double-strand cDNA was digested with Not I and cloned into
the Not I and BcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-lollgo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a
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This sequence belongs to sequence cluster 4215.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?g=CS0BAE012ZF02_AE01071_1&c=4215.r
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(Dases 1 to 924)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)

On May 13, 2003 this sequence version replaced gi:30652931.
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On May 15, 2003 this sequence version replaced gi:30776872. Contact: Genoscope Genoscope Center National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr lst strand cDNA was primed with a Noti-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT & vector. Library was not normalized. Library was constructed by Life Technologies, adivision of Invitrogen.
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                                                                                                                                                                                     This sequence belongs to sequence cluster 4215.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOBAB002ZD11_CS00181_1&c=4215.r
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Pred. No. 2.7e-160;
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                                                                                                                                                                                                                                                                              l. .658
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODE012YJ24"
                                                                                                                                                                                                                                                           Location/Qualifiers
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93.6%;
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Matches 616;
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       synthesis kit
Technologies)."
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1. (Dases I to 658)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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                                                                                                                                                                                      caaractracaraccaacreccaargearcaggaggaggaracrecrecacaaar
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                                                                                714;
         ZAP-cDNA RRT (Life 1
                                                                                Length
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                                                                            Score 609.8; DB 2;
Pred. No. 5.3e-169;
0; Mismatches 37;
         of California, Berkeley) using (Stratagene) and Superscript II
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BX430050
BX430050.2 GI:47003301
                                                                            41.2%;
ilarity 94.3%;
Conservative 0
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                                                                                               Similarity
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Best Local S:
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BX430050/c
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Gaps

599 623 539 683 479

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863 299 923 239 983 179

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On May 15, 2003 this sequence version replaced gi:30778885.

Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoNY sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODE013Y120"
/tissue type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a Not1-oligo(dT) primer. Five prime end enriched,
with a Not1-oligo(dT) primer. Five prime end enriched,
the lot I and ECRNV sites of the pCMVSPORT 6 vector.
Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        division of Invitrogen.
This sequence belongs to sequence cluster 4215.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOBAB002ZG11_CS00184_1&c=4215.r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BX430055 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE013YI20 3-FRIME, mRNA sequence.
BX430055.2 GI:47006728
                                                                                                                                                                                                                                                                                                                                                                                  629 GCACAGAAATAAACA-CCACTTCCGTTTTAGTAGGACCTCTTGTTTCCAATCTGGAAATA 687
                                                                                                                                                                                                                                                                                                                                                                                                         Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                361 Aagaagnaarnrinccaacraacccoonracaroccaccrinragcccracaaaggacrag
                                                                                                                                                                             421 ATCTCTCAAAACTACATGAAACCCTCCGNACCCATACTCGCCTGGNAAGTCTATNNAATA
                                                                                                                                                                                                                                                         TCCCCCTGCACTTCAGGCCATACATTCCAATCCCTGTTCCTGAACAATGGAACAACTTCA
                                              301 cccaacregrargrergarggggggggggggreagarcaggcaagagaaaaaaacargaaa
                                                                                                                                                            449 ITCICICAAAACTACAIGAAACCCICCGTACCCATACTCGCCTGGIGAGCCTATITAAIA
                                                                                                                                                                                                                                     CCACCCTCACTCGGCTCCATGAGGTCTCAGCCCAAAACCCTACTAACTGTTGGATGTGCC
                                                                                    AGGAAGCAATCTCCCAACTGACCCGGGGACATAGCACCCCTAGCGACTAG
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Mammalia, Butheria, Primates, Catarrhini, Hor
1 (bases 1 to 814)
Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Lil-length oDNA libraries and normalization
Unpublished (2001)
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Homo sapiens
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BX430055/c
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                                                                                                                                                                                                                                                                      /tissue_type="PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-olipC(dT) primer. Five prime end enriched,
with a NotI-olipC(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence belongs to sequence cluster 4215.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOBAE011ZH12_AE01057_1&c=4215.r
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                                                                                                                                 03-MAY-2004
                                                                                                                                              Homo sapiens cDNA clone CS0DE012YJ24
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CATCATATAGGAGTTTATCTAAGGGAAACTCCACTTCACTGCCCACACATATGCCCC
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Pred. No. 5.7e-153;
0; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE012YJ24"
                                                                                                                                   ď
                                                                                                                               792 bp
BX409304 Homo sapiens PLACENTA
5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                        BX409304.2 GI:46956516
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88.0%;
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Homo sapiens
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610; Conserv
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AUTHORS
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JOURNAL
COMMENT
                                                                                              RESULT 26
                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                          VERSION
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us-09-319-156b-9.rst

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/tissue_type="foriocarcinoma"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH MGC phage-resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: poTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: poTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: poTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: potantang; Vectoring of the laboratory of placenta; Vectoring the laboratory of Gerald M. Rubin (University of Glifornia, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Pred. No. 2.9e-147;
0; Mismatches 31;
                                                                                                                                                                                                                                                                     1. .586
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:2907101"
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llarity 94.7%;
Conservative C
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BE019603

BASH TO AL NIH MGC 21 Homo sapiens cDNA clone IMAGE:2907101 5'

Similar to TR:096244 095244 ENVELOPE PROTEIN ; contains Alu repetitive element;, mRNA sequence.

BE019603.1 GI:8279682
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                                                     Gaps
                                                     11;
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                         Length 814;
                                                     Indels
                         ; DB 5;
                                                       105;
                         36.3%; Score 537.6;
larity 85.3%; Pred. No. 1.4e
Conservative 0; Mismatches
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Genoscope - Centre National de 1057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 4215.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOAU006ZGO2_U0495_1&c=4215.r.
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                                                                                                                                                                                                                                                             1102 TIGCAAGAICAACTIAACTCCCIAGCAGCAGTAGTCCTTCA-AAATCGAAGAGCTTTAGA 1160
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                                                                                                             241 GGAGTGCTAGGTGCATAGGTACTGGCGTATCACAAACCTCTACTACTCAGTTCTAC 300
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Li (Basea, I to 70.
Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length CDNA libraries and normalization
Onpublished (2001)
On May 22, 2003 this sequence version replaced gi:31018916.
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                                                                                                                                                                                                                                                                                        361 TIGCAAGAICAACTITAACTICCCTAGCAGCAGTAGTICCTITACAAATCGAAGAGCTITAGA
                           181 TATGTCATATCTAAGCCCCGCAACAAAGAGTACCCATTCTTCTTCTTTGTTATAGAGAGA
                                                                                                                                                                         1042 TACAAACTATCTCAAGAAATAAATGGTGACATGGAACAGGTCACTGACTCCCTGGTCACC
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                                                                                                                                                                                                                     301 TACAAACTATCTCAAGAACTAAATGGGGACATGGAACGGGTCGCCGGACTCCCTGGTCACC
/organism="Homo sapiens"
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Homo sapiens
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602593490F1 NIH_MGC_79 Homo sapiens CDNA clone IMAGE:4720846 5',
      C, or G and N = A, C, G, or T). Average insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clonteer. Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
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                                  Uppurizery (127)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.

Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.lln.gov
Plate: LLCM1576 row: c column: 23

High quality sequence stop: 624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol type="max" successions and a daptor sequence: 5. CAGGGCCATATGGC-3 and 3. adaptor sequence: 5. CAGGGCCATATGGC-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            802 ATATITITICICIGIGGIACCICAGCCIAICATIGITIGAAIGGCICTICAGAAICTAIG
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                                                                                          'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                              BG572445.1 GI:13580098
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ilarity 90.5%;
Conservative 0
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                                                            Euteleostomi;
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                                                                                                                                                                                                                                                                           Contract: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
REMPILS: D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD: IMAG958M21530.
RZPDIES: I.M.A.G.E. cDNA Clone Collection;
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq prin
MIST, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
                                                                                                                                                         Neubert, P., Partsch, E.
                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (2018) 1 (2018) 1 (2018) 1 (2018) 1 (2018) 1 (2018) 1 (2018) 1 (2018) 1 (2018) 1 (2018) 1 (2018) 1 (2018) 1 (2018) 1 (2018)
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llarity 95.0%; Pred. No. 3.6e-129;
Conservative 0; Mismatches 26;
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sapiens (human)
                                    Homo sapiens
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/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and ECCRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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IMAGE:3840572 5', mRNA sequence.
CR735592. GI:51584854
EST.
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Pred. No. 4.5e-130;
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Best Local Similarity 83.3%;
Matches 604; Conservative (
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE
Email: seqreté@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a Not1.-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAE021zG07_AE01976_1&c=4215.r
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COT 25-NORMALIZED Homo sapiens CDNA
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Catarrhini, Hominidae; Homo.
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/tissue type="PlaACBNTA COT 25-NORMALIZED"
/tlone lib="Homo sapiens PlaACBNTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PlaACBNTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                             GTCACTGAGAAAGTTAAAAAATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAA
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                                                                                                                                                          727 GICACIGAGAAAGIIAAAGAAAIICGAGAICGAAIACAACGIAGAGCAGGAGCTICGA
                                                                                                                                                                                                       1300 AACACCGAACGCTGGGGCCTCCTCAGCCAATGGATGCCCTGGGTTCTCCCCTTTAGGA
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                 Gaps
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30459619.
Contact: Genoscope
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Pred. No. 3.9e-113;
0; Mismatches 114;
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/db_xref="taxon:9606"
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28.5%;
Best Local Similarity 81.8%;
Matches 535; Conservative 0
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dI) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1000 GGTACTGGCATTGGCAGTATCACAACCTCTACTCAGTTCTACTACAAACTATCTCAAGAA 1059
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                                                                                                                                                                                                                                                                                                           BX365066 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODIO46YA18 3-FRIME, mRNA sequence.
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398 AAATGGGGACATGGAACGGGTCGCCGACTCCCTGGTCACCTTGCAAGATCAACTTAACTC 457
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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1 (Dases 1 to 1071)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)

On May 5, 2003 this sequence version replaced gi:30374869.
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                                                                             Gaps
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Pred. No. 9.2e-120;
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                                                                                                                                                                            GGGAACCTGTTTATTTTAGGGAAGAATGCTGTTAT
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/db_xref="taxon:9606"
/clone="CS0DI046YA18"
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AUTHORS
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For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAA015ZF07_CS01399_1&c=4215.r
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BX37769.2 GI:46272079
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                                                                                                                                                                                  /tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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Pred. No. 1.3e-111;
); Mismatches 97;
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                                                                               1. .890
/organism="Homo sapiens"
                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI022YJ18"
                                                            Location/Qualifiers
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83.7%;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 890)

E Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (201)

On May 2, 2003 this sequence version replaced gi:30342581.

Contact: Genoscope

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1st strand cDNA was primed with a NoII-oligo(dI) primer. Five prime
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into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                       ATGGCCCTCCCTTATCATACTTTTCTCTTTACTGTTCTCTTTACCCCCTTTCGCTCTCACT
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TITLE
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On May 8, 2003 this sequence version replaced g1:30439129.
On May 8, 2003 this sequence version replaced g1:30439129.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE
Email: sequenceGenoscope.cns.fr, Web : www.genoscope.cns.fr
Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                        BX378303
BX378303 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0DI018YH07 3-PRIME, mRNA sequence.
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_list strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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1 (bases 1 to 1058)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization

Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI018YH07"
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Z rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
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/clone=Tissue type="PLACENTA COT 25-NORMALIZED"
/clone=Tis strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
primer. Five prime end enriched, double-strand cDNA was
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                         Euteleostomi;
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                                                                                                                                                                                                  On May 2, 2003 this sequence version replaced gi:30337641
Contact: Genoscope
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                                                                            Craniata; Vertebrata; E
Catarrhini; Hominidae;
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                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertt
Mammalia; Eutheria; Primates; Catarrhini; Hon
1 (bases I to 998)
Li,W. B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 412.2; DB 5;
Pred. No. 2.4e-110;
4; Mismatches 42;
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ilarity 90.5%;
Conservative 4
                                 sapiens (human)
                                                          Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I. (bases 1 to 564)

I.; W. B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

L. Unpublished (2001)

On May 8, 2003 this sequence version replaced gi:30461045.

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Genoscope - Centre National de Sequencage

Z rue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE

Email: seqref@genoscope.cns.fr. Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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BX388917 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI022XJ18 3-PRIME, mRNA sequence.
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316 ATGCAGCGTCCCGGAAATATTGATGCCCCATCGTATAGGAGTCTTTCTAAGGGAACCCCC 375
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                                                  ACCTICACTGCCCACACCCATAIGCCCCGCAACTGCTAIAACTCTGCCACTCTTTGCATG
                                                                              CATGCAAATACTCATTATTGGACAGGAAAAATGATTAATCCTAGTTGTCCTGGAGGACTT
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                                                                                                                                                CATGCAAATACTCATTATTGGACAGGGAAAATGATTAATCCTAGTTGTCCTGGAGGACTT
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/organism="Homo sapiens"
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1 (bases 1 to 905)

2 ii, W.B., Gruber, C., Jessee, J. and Polayes, D.

3 Full-length cDNA libraries and normalization

1 Unpublished (2001)

2 on May 15, 2003 this sequence version replaced gi:30786832.

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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRY sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="Table"Homo sapiens PLACENTA"
/foloe="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
with a NotI-oligo(dT) primer. Five prime end considerable NotI and consubjects of the pcMVSPORT 6; 1st strand cDNA was digested with Not I and cloned into the Not I and cloned into Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                  BX429316 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE013YI20 5-PRIME, mRNA sequence.
                                                                                                                                                  1382 TACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATTG 1441
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                                                     TCAGCCAATGGATGCCCTGGGTTCTCCCCTTCTTAGGACCTCTAGCAGCTCTAATATTGT 1381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence belongs to sequence cluster 4215.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOAT011ZF02_T0974_1&c=4215.r.
Location/Qualifiers
                                                                                                                                                                                 590 TACTCCTCTTTGGACCCTGTATCTTTAACCTTGTTAACTTTGTCTTCTTCCAGAATCG
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                                                                                                                                                                                                                                                                                              530 AAGCTGTAAAACTACAAATGGAGCCCAAGATGCAGTCCAA 491
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Pred. No. 4.1e-110;
0; Mismatches 101;
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division of Invitrogen.
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/tissue_type="PLACENTA"
/clone lib="Homo sapiens PLACENTA"
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Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE012YJ24
mRNA sequence.
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

This sequence belongs to sequence cluster 4215.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODE012DE12NP1&c=4215.r.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 402; DB 5; 1
Pred. No. 2.6e-107;
6; Mismatches 41;
                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 27.1%;
Best Local Similarity 90.0%;
Matches 434; Conservative 6
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3-PRIME, 1
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BX439636 Homo sapiens PLACENTA Homo sapiens CDNA clone CSODE012YJ24 3-FRYBE, mRNA sequence.
BX439636
BX439636.2 GI:47000005
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1 (basea 1 to 1019)
14, W. B., Gruber, C., Jessee, J. and Polayes, D.
Pull-length cDNA libraries and normalization
Ombublished (2001)
On May 15, 2003 this sequence version replaced gi:30771765.
Contact: Genoscope
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/clone=libt strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                                                                Length 564;
                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                 84;
                                                                                                                                                                               Score 406.4; DB 5;
Pred. No. 1.1e-108;
                                                                                                                                                                                                                 0; Mismatches
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larity 84.4%;
Conservative 0
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AUTHORS
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer: Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
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                                                                                                                                                                                                                                                                                                                          division of Invitrogen.
This sequence belongs to sequence cluster 4215.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOBAD005ZE05_AD00422_1&c=4215.r
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                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 484)
14, W.B., Gruber, C., Jessee, J. and Polayes, D.
15, W.B., Gruber, C., Jessee, J. and Polayes, D.
16, W.B., Gruber, C., Jessee, J. and normalization
17, 2001)
18, 2001
19, 2001
19, 2001
19, 2003 this sequence version replaced gi:30766926.
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larity 91.9%; Pred. No. 3.1e-107;
Conservative 0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
   GI:46956493
                                     Homo sapiens (human)
                                                        Homo sapiens
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les 445; Conserv
     3X409035.2
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Sequence Human BAC

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[Dases 1 to 1329]

Baccala,G.P., Pradel,F.K., Bedin,F., Sodoyer,M., Ott,C., Mallet,F.,
Perron,H. and Mandrand,B.

Particular, associated with multiple sclerosis and/or rheumatoid
arthritis, for diagnostic, prophylactic and therapeutic uses

BIO MERIEUX.
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Retroviral nucleic material and nucleotide fragments, in particular, associated with multiple sclerosis and/or rheumatoid arthritis, for diagnostic, prophylactic and therapeutic uses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-UUL-1998 JP 1999508255
07-JUL-1997 FR 97/08816
GLAUCIA PARAHNOS BACCALA, FLORENCE KOMURIAN PRADEL, FREDERIC
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Retroviral nucleic material and nucleotide fragments, in
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Strandedness: Single;
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Perfect score:
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PAT 18-SEP-2002

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Key

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/organism='Unidentified' Location/Qualifiers

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source

FEATURES

AF52050382 AF52050982 AF52051382

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Result No.

1320

PAT 17-AUG-2003

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TITACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAAT 300
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                                                                                                                                                                                                                                                                                                                                                         Unclassified.

1 (bases 1 to 1329)

2 1 (bases 1 to 1329)

3 Perron, H., Beseme, F., Bedin, F., Paranhos-Baccala, G.,

Komurian-Pradel, F., Joilvet. Reynaud, C. and Mandrand, B.

Isolated nucleotide sequences associated with multiple scl.

rheumatoid arthritis and a process of detecting

L. Patent: US 5892703-A 108 24-JUN-2003;

Location/Qualifiers

/organism="unknown"
/mol_type="mRNA"
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Db 1321 CCAGTAACA 1329	RESULT 3 AX001030 LOCUS AX001030 DEFINITION Sequence 12 from Patent WO9902666.	AX001030 AX001030.1 GI:7241266 inidentified	ORGANISM unidentified unclassified. REFERENCE 1 (bases 1 to 1329)	RETROVIRA ASSOCIATE DIAGNOSTI	BIO MERIE	/db_xref="taxon:32644"	Query Match 99.8%; Score 1326; DB 6; Length 1329; Best Local Similarity 100.0%; Pred. No. 0; Matches 1329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1 TCAAAATCGAAGGCTTTAGACTTGCTAACCGCCAAAAGAGGGGAACCTGTTTATTTT 60	OY 61 AGGGGAAGAATGCTGTTAGTATGTTAATCAATCTGGAATCATTACTGAGAAAGTTAAAGA 120	OY 121 AATTTGAGATGGAATATAATGTAGAGGAGCTTTCAAAACACTGCACCTGGGGCCT 180	Oy 181 CCTCAGCCAATGGATGCCCTGGACTCTCCCCTTTAGGACCTCTAGCAGCTATAATATT 240	OY 241 TTACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAAT 300 Db 241 TTACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAAT 300	OY 301 TGAAGCTGTAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA 360	Oy 361 AATCTACCGTGGACCCTGGACGGCCTGCTAGACTATGCTCTGATGTTAATGACATTGA 420	QY 421 AGTCACCCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGG 480 Db 421 AGTCACCCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGG 480	OY 481 AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTCCTGTTGAGA 540	OY 541 GGGTGGACTGAGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCT 600	Oy 601 ANCTGGGAAGGTGACCGCATCCTTTAAACATGGGGCTTGCAACTTAGCTCACCCG 660
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us-09-319-156b-12.rge

TITLE Direct Submission JOURNAL Submitted (16-NOV-2001) DOE Joint Genome Institute, 2800 Mitchell JOURNAL Submitted (16-NOV-2001) DOE Joint Genome Institute, Walnut Creek, CA 94598, USA COMMENT On Nov 16, 2001 this sequence version replaced gi:15383820. On Nov 16, 2001 this sequence version replaced gi:15383820. Draft Sequence Produced by DOE Joint Genome Institute www.jgi.doe.gov Finishing Completed at Stanford Human Genome Center www.shgc.gtanford.edu Quality: Phrap Quality >=40 99.8% of Sequence; Estimated Total Number of Brrors is 0.3. Estimated Total Number of Brrors is 0.3. FEATURES	Query Match	181 117424 117364 301 117304 361	117184 AGTCACCCTCCCGAGGAAATCTCAACTGCACACCCTACTACACTTCCAATTCAGTAGG 480
Db 601 ANCTGGGAAGGTGACCGCATCCTTTAAACATGGGGCTTGCAACTTAGCTCCACCCG 660 ACCAATCAGAGGGTGACCTAAACCTAATCAGGCAAAAACAGGAGGTAAAGCCATAGCC 20 1 1 1 1 1 1 1 1 1	Qy 901 CTCAAGCTGAGCTTTGTTCGCCATCCACTGCTGTTTGCCACCACACACCCGCT 960 Db 901 CTCAAGCTTTTGTTCGCCATCCACTGCTGTTTGCCACCGTCACACACCGCT 960 CTCAAGCTTTTGTTCGCATCCACCACTGTTTGCACCGTCACCGGCG 960 Qy 961 GCTGACTTCCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGCGAGGT 1020 Db 961 GCTGACTTCCATCCCTTTGGATCCAGCAGAGTGTCCATGTCCTCGATCGCAGGAGT 1020 Qy 1021 ACCCATTGCCACTCCCGATCAGGCTAAGAGTGCTCTGCATGGCTAAGTGCC 1080 Db 1021 ACCCATTGCCCAGTCAGGCTTACATGCTTCCTTGCATGGCTTAAGTGCC 1080 Qy 1081 TGGGTTTGTCCTAATAGAACTGGTCACTGGCTTCCATGGTTCCTTCC	Qy 1141 CCACGGCTTCTAATAGAGCTATAACACTCACCGCAAGATTCCATTCCTTGGTA 1200 Db 1141 CCACGGCTTCTAATAGAGCTATAACACTCACGCATGGCCCAAGATTCCATTCCTTGGTA 1200 Qy 1201 TCTGTGAGGCCAAGAACCCCAGGTCAGAGAANGTGAGGCTTGCCACCATTGGGAAGTGG 1260 Db 1201 TCTGTGAGGCCAAGAACCCCAGGTCAGAGAANGTGAGGCTTGCCACCATTTGGGAAGTGG 1260 Qy 1261 CCCACTGCCATTTGGTAGCGGCCCACCACCATCTTGGGAGCTGTGGGAGGAAGGA	RESULT 4 AC093531 LOCUS DEFINITION Home sapiens chromosome 5 clone RP11-405L7, complete sequence. ACCESSION AC093531 AC093531.2 GI:16945981 FIGWARDS HOME sapiens (human) ORGANISM HOME sapiens (human) ORGANISM HOME sapiens (human) ORGANISM HOME sapiens (human) ORGANISM HOME Sapiens (human) ORGANISM HOME Sapiens (human) ORGANISM HOME Sapiens (human) ORGANISM HOME Sapiens (human) ORGANISM LOCUSTAIL (bases 1 to 163803) TITLE JOURNAL Direct Submission JOURNAL Direct Submission JOURNAL Submitted (31-AUG-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center. Submitted (31-AUG-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

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join (247. .811,7440. .9669)
/product="envelope glycoprotein"
/note="putative mRNA transcript 2"
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/note="putative mRNA transcript 3"
/note="putative mRNA transcript 3; no coding region"
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'isolation_source="PBMC of orangutan 1"
                                             /note="isolated by PCR; ERVWE1 locus,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
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Submitted (06-MAY-2002) Retrovirology Department, UMR 2142
Submitted (06-MAY-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee d'Italie, Lyon 6744 cedex 07, France
Location/Qualifiers
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Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G., Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWEl is a bona fide gene: in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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/mol type="genomic DNA"
/isolate="1"
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Mallet, F., Bouton, O. and Oriol, G.
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AUTHORS
TITLE
JOURNAL
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                                                              Direct Submission
Direct Submission
Direct Submission
Submitted (28-NOV-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94589, USA
Drave, Walnut Creek, CA 94589, USA
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
Www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.7.
Direct Submission
Submitted (07-SEP-2002) DOE Joint Genome Institute, 2800 Mitchell
Dive, Walnut Creek, CA 94598, USA
3 (bases 1 to 14871)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Pred. No. 0;
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ilarity 88.9%;
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Homo sapiens chromosome 5 clone RP11-120B7, complete seguence.
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1 (bases 1 to 148711)

DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                      ACCAATCAGAGGGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCC
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DOE Joint Genome Institute and Stanford Human Genome Center.
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FLGPHAAIILLLEGPCTRYNLVNFVSSRIBAVKLQMEBFRMGSKTKIYRRPEDDLTAB
RSDVNDIKCTPPBEISAAQPLLRPNSAGSS"
Loses 1 to 2694)
Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWEI is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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                                                                                                                                                                    [bases 1 to 2694)
Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMeritux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 6934 cedex 07, France
Location/Qualifiers
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/note="splice acceptor site"
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FLGPLEDRAFALILLLEFGECTFRILLVNFVSSRIRAVKLQMEPKMQSKTKIYRRPLDRRPASP
                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2694)

Mallet, F., Bourdon, O., Prudhomme, S., Cheynet, V., Oriol, G., Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.

The endogenous retroviral locus ERVWEl is a bona fide gene involve in hominoid placental physiology

Proc. Natl. Acad Sci. U.S.A. 101 (6), 1731-1736 (2004)
                                                                                                                                                                                                                             Dases 1 to 2694)
Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMeriatux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 6934 cedex 07, France
Location/Qualifiers
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0; Mismatches 110;
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1603 CCTCAGCCAATGGATGCCTGGATTCTCCCCTTCTTAGGACCTCTAGCAGCTATAATT 1662 1423 TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCTGAAAGAGGGGGAACCTGTTATTTT 1483 AGGGGAAGAATGCTGTTATTATGTTAATCAATCCGGAATCGTCACTGAGAAGTTAAAGA 61 AGGGGAAGAATGCTGTTAGTATGTTAATCAATCTGGAATCATTACTGAAAAGAAGGTTAAAGA 121 AATTTGAGATCGAATATATGTAGAGCAGAGGACCTTCAAAACACTGCACCCTGGGGCCT 1543 AATTCGAGATCGAATACAACGTAGAGCAGAGAGCTTCGAAACACTGGACCCTGGGCCT 1 TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTT Gaps 13; Indels ð g à

Ar>20489S2 2694 bp DNA linear PRI 11-FEB-2004 Complete cds, and 3' long terminal repeat, complete sequence. AF520490

RESULT 9 AF520489S2 LOCUS DEFINITION

AF520490.1 GI:33410948

ACCESSION VERSION KEYWORDS

Length 2694;

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AF520505S2 2694 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 37 allele A, envelope glycoprotein gene,

RESULT 10 AF520505S2 LOCUS DEFINITION

1482 Bukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2694)
Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWEl is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004) 1542 120 180 181 CCTCAGCCAATGGATGCCCTGGACTCTCCCTTTAGGACCTCTAGCAGCTATAATATT 240 1423 TCAAAATCGAAGAGCTTTAGACTTGCTAAACGCCTGAAAGAGGGGGAACCTGTTTATTTT 1483 AGGGGAAGAATGCTGTTATTATGTTAATCAATCCGGAATCGTCACTGAGAAGTTAAAGA TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTT AGGGGAAGAATGCTGTTAATGTTAATCAATCTGGAATCATTACTGAGAAAGTTAAAGA AATTTGAGATCGAATATAATGTAGAGCGAGAGGACCTTCAAAACACTGCACCTGGGGGCCT Gaps complete cds, and 3' long terminal repeat, complete sequence. AF520506 AF520506.1 GI:33410980 UMR 2142 - 46 allee Length 2694; 13; Maller, F., Bouton, O. and Oriol, G. Direct Submission.

Submitted (O'-JUN-2002) Retrovirology Department, CNRS-bioMerieux, Ecole Normale Superieure de Lyon d'Italie, Lyon 69364 cedex 07, France Location/Qualifiers Indels 78.0%; Score 1036.8; DB 9; larity 90.2%; Pred. No. 9.7e-305; Conservative 0; Mismatches 110; Ā /cell_type="PBMC's" /note="endogenous_virus: HERV-W" /mol_type="genomic_DNA"
/mol_type="genomic_DNA"
/isolate="individual 37 allele
/db_xref="taxon:9606"
/chromosome="7" 1705. .1720 /note="splice acceptor site" 1959. .2694 /note="splice acceptor site" 284. .1900 1. .2694 /organism="Homo sapiens" note="syncytin" /map="7q21-q22" /sex="male" (bases 1 to 2694) (human) 43. .57 2 of 2 Homo sapiens Homo sapiens Best Local Similarity Matches 1134; Conserv misc_feature 121 1543 ઠે g Š

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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2694)
Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWEI is a bona fide gene involved
                                                                                                     PRI 11-FEB-2004
                                                                                              AF520483S2
Homo sapiens individual 147 allele B, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
2610 TCCATAAGGCCAAGAACCCCAGGTCAGAGAACACGAGGCTTGCCACCATCTTGGGAG 2666
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (107-JUN2-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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/cell_type="PBMC's"
/note="endogenous_virus: HERV-W"
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/isoTate="individual 147 allele
/db_xref="taxon:9606"
/chromosome="7"
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                                                                                                      2694 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 148 allele B, envelope glycoprotein gene, AF520488
                                                                                                                                                                                                                                                                                                                                                                                                       involved
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bumanlai; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 2694)
Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWE1 is a bona fide gene involve in hominoid placental physiology Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Maller,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMeriaux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 6934 cedex 07, France
Location/Qualifiers
                                2610 TCCATAAGGCCAAGAACCCCAGGTCAGAGAACACGAGGCTTGCCACCATCTTGGGAG
             TCTGTGAGGCCAAGAACCCCCAGGTCAGAGAANGTGAGGCTTGCCCACCATTTGGGAAG
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Pred. No. 3e-304;
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/note="splice acceptor site"
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GNIDAPSYRSLSKGTPTFTAHTHMPRNCYRSATLCHANTHWTGWAINPSCFGGIGY
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Pred. No. 3e-304;
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Direct Submission
Submitted (07-JUN-2002) Retrovirology Department,
CNRS-bioMerieux, Ecole Normale Superieure de Lyon
d'Italie, Lyon 69364 cedex 07, France
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TGGGTTTGTCCTAATAGAACTGAACACTGGTCACTGGGTTCCATGGTTCTCTTCCATGAC 1140	2694 bp DNA linear PRI 13. long terminal repeat, complete seq 13. long terminal repeat, complete seq 1410960 Day Chordata; Craniata; Vertebrata; Eut 14. primates; Catarrhin; Hominidae; Hos 14. primates; Catarrhin; Hominidae; Hos 14. primates; Catarrhin; Mominidae; Hos 14. primates; Catarrhin; Mominidae; Hos 14. primates; Catarrhin; Mominidae; Hos 14. primates; Lack Lack Lack Mandrand, B. scrioviral locus ERVWE1 is a bona fide 9 erroviral physiology Scrib 1731-1736 (2004) 10. and Oriol, G. and Oriol, G. and Oriol, G. and Oriol, G. and Oriol, G. and Oriol, G. and Oriol, G. and Oriol, G. and Oriol, G. and Oriol, G. and Oriol, G. and Oriol, G. and Oriol, G. and Oriol, G. and Oriol, G. and Oriol, G. and Oriol, G. and Oriol, Retrovirology Department, UMR 2	blowerieux, Ecole N lication/Qualif Location/Qualif lication/Qualif lication/Qualif lo	284. 1900 /note="syncytin" /codon_start=1 /codon_start=1 /codon_start=1 /product="envelope glycoprotein" /protein_id="AAQ17570.1" /db.xref="cd1:334.096." /translation="MALPYHIELFTULDESFTLTAPPPCRCWTSSSPYGEFLWRMQRP /translation="MALPYHIELFTULDESFTLTAPPPCRCWTSSSPYGEFLWRMQRP GNIDAPSYRSLSKGTPTFTAHTHMPRNCYHSATLCWHANTHYWTGKMINPSCPGGLGV TVCWTYFTGYGGMSDGGGGVGDQAREKHVKEV1SQLTRVHTSSPYGSIDLSKLHETLRT HTRLVSLFNTTLTGLHEVSAQNPTNCWTCSOTTRVHTPPTQ1VCBGIFFCVGTSA YRCHNGSSESWCFLSFLVPPWTYTTRODLYSYVISKPRNRVPILPPTQ1CAGVLGALG TG1GGITTSTQFYYKLSQELNGDMERVADSLVTLQDQLNSLAAVULQNRRALDLLTAE RGGTCLFGEECCYTVNGGSTVTBRVKETRDRIQRRAEBELRNTGPWGLLSQWNFWILP FLGPLAAIILLLFGPCIFNLLVNFVSRRIEAVKLQMEPRAQSKTKIYRRPLDRRASP RSDVNDIKGTPPEELSAAQPLLRPNSAGSS" /note="splice acceptor site" 17592694
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RGGTCLFLGEBECCYYNDSGIVTEKVKEIRRIGARALDLITAE
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Cranrhini; Hominidae; Homo.

1 (bases 1 to 2694)
Maller,F. Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWE1 is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
                                                                                                                                    CCACGGCTTCTAATAGAGCTATAACACTCACCGCATGGCCCCAAGATTCCATTCCTTGGTA 1200
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Direct Submission
Submitted (Or-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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/organism="Homo sapiens"
/mol type="genomic DNA"
/isolate="individual 30 allele
/db.xref="taxon:9606"
/chromosome="7"
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/note="Caucasian
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/sex="female"
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0; Mismatches 111; Indels
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/note="syncytin"
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/note="splice acceptor site"
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Homo sapiens individual 45 allele A, envelope glycoprotein gene,
complete cds, and 3' long terminal repeat, complete sequence.
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Direct Submission
Submitted (O7-JTM-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 63344 cedex 07, France
Location/Qualifiers
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The endogenous retroviral locus ERVWE1 is a bona fide gene in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G., Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
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Direct Submission
Submitted (OrJ-JUN-2002) Retrovirology Department,
CNRS-blowerieux, Ecole Normale Superieure de Lyon
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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TICGAGCCGGCAACGGCAACCCCCTTTGGGTCCCCTCCTTTGTATGGGAGCTCTGTTTT
                                   CACTCTATTTCACTCTATTAAATCATGCACTCCACTCTTCTGGTCCGTTTTTTATGG
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Mallet,F., Bouton,O. and Oriol,G.
Mallet,F., Bouton,O.
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 6934 cedex 07, France
Location/Qualifiers
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/mol type="genomic DNA"
/isoTate="thatvidual 49 allele
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Pred. No. 3e-304;
0; Mismatches 111; Indels
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Best Local Similarity 90.1%;
Matches 1133; Conservative (
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2694 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 55 allele A, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence. AF520518
AF520518.1 GI:33411004
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 2694)
Mallet, F., Boucotte, G., Prudhomme, S., Cheynet, V., Oriol, G.,
Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
The endogenous retroviral locus ERVWEI is a bona fide gene involve in hominoid placental physiology
Proc. Natl. Acad Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department,
CNRS-bioMeriteux, Ecole Normale Superieure de Lyon
d'Italie, Lyon 63364 cedex 07, France
Location/Qualifiers
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Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2694)
Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G., Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWEI is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Homo sapiens individual 55 allele B, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
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Direct Submission

Submitted (Or-JUN-2002) Retrovirology Department, UMR 2142

CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee d'Italie, Lyon, 69364 cedex 07, France
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/note="splice acceptor site"
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               note="splice acceptor site"
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                                                     note="syncytin"
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AF520521S2
Homo sapiens individual 6 allele A, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
AF520522
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mallet,F., Bouton,O. and Oriol,G.
Mallet,F., Bouton,O. and Oriol,G.
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMeriaux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWEI is a bona fide gene in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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/organism="Homo sapiens"
/mol type="genomic DNA"
/isolate="individual 6 allele
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Pred. No. 3e-304;
0; Mismatches 111; Indels
/sex="female"
/cell_type="PBMC's"
/note="endogenous_virus: HERV-W"
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/note="splice acceptor site"
1959. .2694
                                                       'note="splice acceptor
                                                                                   'note="syncytin"
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Best Local Similarity 90.1%;
Matches 1133; Conservative
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1 (bases 1 to 2694)
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Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
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Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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2610 TCCATAAGGCCAAGAACCCCAGGTCAGAGAACACGAGGCTTGCCACCATCTTGGGAG 2666
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Homo Bapiens individual 65 allele A, envelope glycoprotein gene,
complete cds, and 3' long terminal repeat, complete sequence.
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Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 6934 cedex 07, France
Location/Qualifiers
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43. 57
xref="taxon:9606"
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1 (bases 1 to 2694)

Mallet,F.; Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G., Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B. decotte,G., Duret,L. and Mandrand,B. decotte,G., Duret,L. and Mandrand,B. decotte,G., Duret,L. and Mandrand,B. decotte,G., Duret,L. and Mandrand,B. decotte,G., Duret,L. and Mandrand,B. decotte,G., Duret,L. and Mandrand,B. decotte,G., Duret,L. and Mandrand,B. decotte,G., Duret,L. and Mandrand,B. decotte,G. decotte,G.
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Pred. No. 3e-304;
0; Mismatches 111; Indels
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                                             /organism="Homo sapiens"
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/isolate="individual 65 allele
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Homo sapiens individual 80 allele B, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2694)
Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWEl is a bona fide gene involvent hominoid placental physiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2011 AGCTGGGAAGGTGACCACATCCACCTTTAAACACGGGGCTTGCAACTTAGCTCACACGTG
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                                                                    541 GGGTGGACTGAGAGAGAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCCNAAGCCT
                                                                                     601 ANCTGGGAAGGTGACCGCATCCATTTAAACATGGGGTTGCAACTTGAGCTCGCG
                                                                                                                                                                 ACCAATCAGAGAGCTCACTAAAATGCTAATCAGCAAAAACAGGAGGTAAAGCAATAGCC
                                                                                                                                                                                       2071 ACCAATCAGAGAGCTCACTAAATGCTAATTAGGCAAAGACAGGAGGTAAAGAAATAGCC
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                       AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTCCTGTTGAGA
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AGTCACCCCTCCCGAGGAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGG
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Pred. No. 3e-304;
0; Mismatches 111; Indels
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1959. .2694
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/sex="male"
/cell_type="PBMC's"
/note="Caucasian
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note="syncytin"
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Homo sapiens individual 81 allele A, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
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GATCTACCGCAGACCCCTGGCCGCCTGCTAGCCCACGATCTGATGTAATGACATCAA 1830
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bukarychai, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2694)
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                                       2131 AATCATCTATTGCCTGAGAGCACAGCAGGAGGACAATGATCGGGATATAAACCCAAGTC
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1071 ACCAATCAGAGAGCTCACTAAAATGCTAATTAGGCAAAAACAGGAGGTAAAGAAATAGGC
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                                                                                                                                             1891 AAGCAGTTAGAGCGGTCGTCGGCCAACTCCCCAACAGCACTTAGGTTTTCCTGTTGAGA
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           (6), 1731-1736 (2004)
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1 2 (bases 1 to 2694)
2 (bases 1 to 2694)
5 Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
1 Submitted (07-JUN-2002) Retrovirology Department, UMR CNRS-bioMorieux, Ecole Normale Superieure de Lyon - 4' (1alie, Lyon 69364 cedex 07, France Location/Qualifiers
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Homo sapiens individual 95 allele A, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.

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                                                 AAGCAGTTAGAAGCGGTCGTCGGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAG
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                      AATCTACCGTGGACCCCTGCCTGCTAGACTATGCTCTGATGTTAATGACATTGA
                                                                                                                  AGTCACCCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGG
                                                                                                                                                                                                              481 AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTCCTGTTGAGA
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Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWE1 is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Mallet, F., Bouton, O. and Oriol, G.
Direct Submission
Submitsed (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 alle
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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/mol_type="genomic DNA"
/isolate="individual 81 allele A"
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Oy 101 TGAAGCTGTAAAACTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA 360 1723 CGAAGCTGTAAAACTACAAATGGAAGCCCAAGATGCAGTCCATGACTAA 1770 Oy 361 AATCTACCGTGACCGCTGCTGACTGACTATGCTCTGATGTTAATGACATTGA 420 1771 GATCTACCGCAGACCGCCTGCTGACCTACACTCTGATGTTAATGACATTGA 420 Oy 421 AGTCACCGCAGACCCCTGGACCGCCTGCTACACACACTCAATTCAGTAG 480 Db 1831 AGGCACCCTCCCGAGGAAATCTCAACTGCACACTACACT			Qy 1081 TGGGTTTGTCCTAATAGAACTGAACACTGGTTCCTTGCTTG	'AF52055382 AF52055382 2694 bp DNA linear PRI 11-FEB-2004 LOCUS Homo sapiens individual 96 allele A, envelope glycoprotein gene, Complete cds, and 3' long terminal repeat, complete sequence. ACCESSION AF520554 VERSION AF520554.1 GI:33411076 KEYWORDS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2694) AUTHORS Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G., Bonnaud,B., Lucotte,G., Durect,L. and Mandrand,B. TITLE in hominoid placental locus ERVWEL is a bona fide gene involved in hominoid placental physiology Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004) PUBMED 14757826 Chases 1 to 2694) AUTHORS Mallet,F., Bouton,O. and Oriol,G. TITLE Direct Submission O. and Oriol,G.	FEATURES G. ICALIE, Dyon 9534 Cedex 07, Flance Source 1. 2694 r. 2694 r. 2696 r. 2694 r. 2696 r. 2694 r. 2696 r. 2694 r. 2696 r. 2694 r. 2696 r. 2694 r. 2696 r. 2694 r. 2696	pe glycoprotein" 11069" 1297.1" 11069" 127HTHPRNCYHSATLCHANTHYMGKNINPS GVODAREKHVENCYHSATLCHANTHYMGKNINPS GVODAREKHVENCYHSATLCHANTHYTTSSCHOLDLE EUVENSMYTTNSGCTRWTPENGLDLENNFST LUVENSMYTTNSGCTRWTPENGLOLDENNFST LUVENTYTTNSGCTRWTPENGLOLDENNFST LUVENTYTTNSGCTRWTPENGTUCLENNRET LUVENTYTTNSGCTRWTPENGTUCLESGIF LUVENTYTTNSGCTRWTPENGTUCLESGIG CHOLDLWEVSERIEAVLONGLAAVLONREA GOGIGGONGSTERNYGERGERNTGPWGLLSG CHOLLUNFUSSRIEAVLONREAELRNTGPWGLLSG CHOLLUNFUSSRIEAVLONREAERNTGPWGLLSG CHOLLUNFUSSRIEAVLONREPKWGSKTKIYRRP CEPLOR site" TE 1035.2; DB 9; Length 2694; d. No. 3e-334;	MACCHES 1133; CORRELYATIVE U; MISMACCHES 111; INVELS 1.5 CORRECT TATATITIT 60 1 TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAGAGGGGGAACCTGTTTATTTT 60 1423 TCAAAATCGATTAGTATGTTAACCACTGAAAAGAGGGGAACCTGTTTATTTT 14 1483 AGGGAAGAATCGTTTAGTATGTTAATCAATCTGGAATCATTACTGAAAAGTTAAAGA 12 121 AATTTGAGATCGTTTATTATGTTAATCCATCGGAATCGTCACTGGGGGCT 18 121 AATTTGAGATCGAATATAATGTAGAGCAGGGACCTTCAAAACACTGGGGGCCT 18 1543 AATTCGAGATCGAATACAACGTAGAGCAGGGAGCTTCGAAAACACTGGGGCCT 16	Db 1603 CCTCAGCCAATGGATGCCTGGATTCTCCTTTTTAGGACCTCTTGGAGTTTTTTTT

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Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMeritux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69344 cedex 07, France
Location/Qualifiers
                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. I dases I to 2694)
Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G., Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
The endogenous retroviral locus ERVWEl is a bona fide gene in hominoid placental physiology in hominoid placental physiology Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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0; Mismatches 111; Indels
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/note="syncytin"
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RSDVNDIKGTPPEEISAAQPLLRPNSAGSS"
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Mallet,F.; Bouton,O.; Prudhomme,S.; Cheynet,V.; Oriol,G.;
Bonnaud,B.; Lucotte,G.; Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWE1 is a bona fide gene involve in hominoid placental physiology
Proc. Natl. Acad Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Pred. No. 3e-304;
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Direct Submission
Submitted (O'JUN-2002) Retrovirology Department,
CNRS-blowerieux, Ecole Normale Superieure de Lyon
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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                                                                                                                                                                                                          1663 GCTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAACTTTGTCTTCCTGGAAT
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                                                                      CCTCAGCCAATGGATGCCTGGACTCTCCCCTTCTTAGGACCTCTAGCAGCTATAATATT
                                                                                                                                                                    241 ITTACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAAT
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284. .1900
/ note="syncytin"
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1 (Bases I to 268)

1 (Bases I to 268)

Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G., Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.

The endogenous retroviral locus ERVWEI is a bona fide gene involved in hominoid placental physiology

Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
                            AF520563S2 2694 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 71 allele B, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submission

Direct Submission

CNRS-biomerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69364 cedex 07, France

Location/Qualifiers
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90.1%; Pred. No. 3e-304;
ive 0; Mismatches 111; Indels 13;
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/isolace="taxon:9606"
/chromosome="7"
/map="7q21-q22"
/map="7q21-q22"
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1705. 1720
//note="splice acceptor site"
1959. .2694
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/organism="Homo sapiens"
                                                                                                                           AF520564.1 GI:33411096
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Homo sapiens (human)
Homo sapiens
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Best Local Similarity 90.1
Matches 1133; Conservative
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VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM
         AF520563S2
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AUTHORS
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Human BAC clone RG083M05 from 7q21-7q22, complete sequence.
AC000064
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 56093)
Pauley,A.
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AATCATCTATTGCCTGAGAGCACAGGGGAAAGGACAAGGATTGGGATATAAACTCAGGCA
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                                              ACCAATCAGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCC
                                                                                                                                                                   TTCAAGCCAGCAACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTT
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Unpublished (1996)
2 (bases 1 to 56093)
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      St. Louis, MO 63108, uca
e-mail: sapiens@watson.wustl.edu
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Submitted (13-NOV-1996)
Genome Sequencing Center
Department of Genetics, W
St. Louis, MO 63108, USA
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         2610 TCCATAAGGCCAAGAACCCCAGGTCAGAGAACACGAGGCTTGCCACCATCTTGGGAG 2666
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Pred. No. 3.2e-304;
0; Mismatches 111;
                                                                                     DNA
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gene sets
Patent: WO 0194629-A 81 13-DEC-2001;
Avalon Pharmaceuticals (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                           1. .56093
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                  AX329572 56093 bp
Sequence 81 from Patent WO0194629.
SX329572
AX329572.1 GI:18102550
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.1%;
Matches 1133; Conservative (
                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                             Homo sapiens (human)
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47898. .48115
/note="match to human 5' EST H62306 (NID:g1015138), bases
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/note="match to human 3' EST N29952 (NID:g1148472), bases
290-455, and 5' EST R12730 (NID:g765806)"
                                                                                                                                                           13794. .13877
/rpt_family="ALU"
13878. .13906
//gene="WUGSC:H_RG083M05.1"
/note="match to human 5' EST H41382 (NID:g917434), bases
30-58"
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/ rpt family="ALU"
complement(49406. .49534)
/nore="match to human 3' EST R65794 (NID:g838432), bases
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note="match to human 3' EST H48898 (NID:9988738), bases
                     complement(12612. .12907)
/rpt_family="ALU"
13670. .13793
/gene="WIGSC1R RG083M05.1"
/note="match to human 5' EST H41382 (NID:917434), bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similarity to various SS-RNA virus polyproteins; pseudogene; region of matches and close matches to multiple human ESTs, see R68740 (NID:9842257)"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="ALU"
1867. .19235
/note="match to human fetal brain 5' EST D61494
(NID:9970409), bases 1-255, and to human 3' EST R07476
(NID:9759399)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (46107. 47026)
/note="match to multiple human ESTB, see N81064
(NID:g1243765), H48897 (NID:g988737), and M78831
(NID:g273146)"
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/note="match to multiple human BSTB, see N30113
(NID:g1148633)"
39800. .40085
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/note="match to multiple human ESTs, see W37495
(NII:g1319089)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37316. .37489
/note="Grail prediction, score = 80"
/evidence=not experimental
complement (38938. .39224)
/rpt family="ALU"
39225. .39707
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complement (42283. .42891)

/rpt_family="ALU"

complement (45474. .45613)

/rpt_family="ALU"

complement (45614. .45737)
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complement 40632, 40924)
/rpt_family="ALU"
42891)
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complement(15618. 15907)
/rpt_family="ALU"
17227. 17522
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/rpt_family="ALU"
complement (47365. .47782)
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/rpt family="ALU"
complement (48406. .48584)
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/rpt_family="ALU"
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/rpt_family="ALU"
complement(14110.
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/rpt_family="ALU"
21507. .37303
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/ Ab xref="G1:1669371"

/ Ab xref="G1:1669371"

/ Ab xref="G1:1669371"

/ Armalation="KRLENIQKTEVARSEAVWMQPSVVLLDDLDLIAGLPAVPEHEH
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SRQSISTREKLVLTTLDFQKALRGFLPASLRSVNLHKPRDLGMDKIGGLHEVRQILMD
TIQLPAKVCLKKEKYPELFANLFIRQKATGLLYFPOFFGTGKTLLAGVTARRESRNFTSV
KGPELLSKYIGASEQAVRDIFIRQKARKPCILFPDEFESIAPRRGHDNTGYTDRVVNQ
LLTQLDGVRGLGGGVYVLATASRSPBLLDPALLRRGRLDKCVYCPPPDQVTISYLESKTQ
QMLASFLVSRLEILNVLADSSLPLADDVDGHVASYTDSFTGADLKALLYRAQLEALHG
MLLSKWGEILDPDESKFNMYRLYFGSSYESELGNGTSSDLSSQCLSAPSSMTQDLPGVP
GKDQLESQPPVLRTASGSCGELTQBCRDGCOGLTQBCRDGSSNGQPGPI
KTRLAISQSHLMTAAGHTRFSISEDDWKNFAEL"
                                                                                                                                                                                     This clone is from the first release of the human BAC library. The library contains cloned DNA from a human male fibroblast cell line 9785K. For references see: Shizuya et al., Proc. Natl. Acad. Sci. 89:8794-8797 (1992); Kim et al., Genomics 34:213-218 (1996).
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/gene="WUGSC:H_RG083M05.1"
/note="match to human 5' EST N22627 (NID:g1130501), bases
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note="match to human 3' EST H75782 (NID:g1049794), bases
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This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                     NEIGHBORING SEQUENCE INFORMATION:

He orientation of this clone is unknown. Actual start of this clone is at base position 1 of H_RG083M05; actual end is at 56093 of H_RG083M05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="WUGSC:H_RG083M05.1"
/note="ATPPase; atrong similarity to peroxisome
blosynthesis protein PAS1 (PID:g1172019); coded for by
human cDNA C04279 (NID:g1467530)
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/gene="WUGSC:H_RG083M05.1"
/note="match to human 5' EST H75921 (NID:g1050050),
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/rpt family="ALU"
complement (581. 7133)
/rpt family="L1"
complement (7767. 8037)
/rpt family="ALU"
complement (8186. 8472)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L. .56093
/organism="Homo sapiens"
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8473. .8625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone contains STS BWSS1725
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/db_xref="taxon:9606"
/chromosome="7"
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37906 CTTGAGCTGAGCTTTCGCTCGCCATCCACCACTGCTGTTTGCCGCCACCGCAGACCCGCC 37965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149194 bp DNA linear PRI 01-MAR-2002
Homo sapiens BAC clone CTB-10G5 from 7q21-7q22, complete sequence.
AC007566.
HTG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AATCATCTATTGCCTGAGAGCACAGCGGGAAAGGACAAGGATTGGGATATAAACTCAGGCA
                                                                                                                                                                                                                                                          ACCCATTGCCACTCCCGATCAGGCTAAAGGCTTGCCATTGTTCCTGCATGGCTAAGTGCC
                                                                                                                                                                                                                                                                                                                  CACTCTATTTCACTCTATTAAATCATGCAACTGCACTCTTCTGGTCCGTGTTTTTTATGG
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Sulston,J.B. and Waterston,R.
Sward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 149194)
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AC007566/c
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          309-440"

complement (49638. .49672)

/rpt_family="ALU"

/rpt_family="ALU"

complement (49674. .49890)

/note="match to human 3 ' EST N29952 (NID:g1148472) and

EST N29938 (NID:g1148458), sequences are from opposite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37018 TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCTGAAAGAGGGGGGAACCTGTTTATTTT
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                                                                                                                                                    Complement (49698 . .51806)
/gene="WUGSC:H_RG083M05.2"
complement (join (49698 . .49888,51575. .51806))
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R65891 (NID:g838529), R65794 (NID:g838432) and R65794
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Pred. No. 3.2e-304;
0; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                              complement (51576 .51759)
/gene="WudScr! H RG083M06.2"
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55557. .55843
                                                                                                                                   ends of the same clone"
complement (49698. .5180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.1%;
Matches 1133; Conservative
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COMMENT

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note="match to EST AA425526 (NID:92106267) zw48b03.rl"
8719. .3785
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/note="similar to Mus musculus EST BB253526
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1542. .3628
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                        CTB-10G5 contains the entire sequence of CTB-83M5 Location/Qualifiers
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2248. .2388
2248. .2388
2248. .2387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="match to EST BE272564 (NID:g9146913)"
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/note="match to EST AW579261
2248. 2387
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/chromosome="7"
                                                                                                                                                                                                                                         'clone lib="CITB-978SK-B"
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3108. .3392
/rpt_family="Alu"
3540. .3628
                                                                                                                                                                                                                      clone="CTB-10G5"
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3719. .3785
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                                                       FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE INFORMATION:
Clone CTB-10G5 is from the first release of the human BAC library
CITB-9788X-B. The library contains cloned DNA from the male
fibroblast cell line 9788X. See: Shizuya et al., Proc. Natl. Acad.
Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8
(1996), This clone is available from Research Genetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA 5 (bases 1 to 149194)
                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (06-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
B (bases 1 to 149194)
                                                                                                                                                 Submitted (16-NOV-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 53108, USA 6 (base 1 to 149194) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                    Louis,
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The clone sequenced to the left is RFS-911H5, 200 base pair
overlap. Actual start of this clone is at base position 195 of
CTB-10G5; actual end is at base position 150532 of CTB-10G5.
                                                                                                                                                                                                                                                                                Submitted (03-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA 7 (bases 1 to 149194) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_RG010G05
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(http://www.resgan.com).
vrcTOR: pBeloBAC11
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                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                         Direct Submission
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	RESULT 35 AF5204852 LOCUS DEFINITION Home sapiens individual 148 allele A, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence. ACCESSION VERSION KEYWORDS SEGMENT 2 of 2 SEGMENT CORDINATE Home sapiens (human) ORGANISM Home sapiens (human) REFERENCE Home sapiens (human) ORGANISM Home sapiens (human) REFERENCE Home sapiens (human) ORGANISM Home sapiens (human) AUTHORS Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Home. REFERENCE Home sapiens (human) ORGANISM REFERENCE AUTHORS Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G., Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B. TITLE Home cadogenous retreviral locus ERWME1 is a bona fide gene involved in hominoid placental physiology JOURNAL POOR MAILET, Bouton, O. and Oriol, G., 1731-1736 (2004) AUTHORS Mallet, F., Bouton, O. and Oriol, G. TITLE Direct Submission CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee d'Italie, Lyon 69346 cedex 07, France d'Italie, Lyon 69346 cedex 07, France A'Italie, Lyon 69346 cedex 07, France d'Italie, Lyon 69346 cedex 07, France A'Italie, Lyon 69346 cedex 07, France A'Italie, Lyon 69346 cedex 07, France A'Italie, Lyon 69346 cedex 07, France A'Italie, Lyon 69346 cedex 07, France A'Italie, Lyon 69346 cedex 07, France A'Italie, Lyon 69346 cedex 07, France A'Italie, Lyon 69346 cedex 07, France A'Italie, Lyon 69346 cedex 07, France A'Italie, Lyon 69346 cedex 07, France A'Italie, Lyon 69346 cedex 07, France A'Italie, Lyon 69346 cedex 07, France A'Italie, Lyon 69346 cedex 07, France A'Italie, Lyon 69346 cedex 07, France A'Italie, Lyon 69346 cedex 07, France A'Italie, Lyon 69346 cedex 07, France
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Homo sapiens (human)
Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2694)
Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWEI is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submitssion
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CURS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
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TRCLNGSSESWMFLSFLVPPWTIYTTGDDLYSYVISKPRNRRVPILPFVIGAGVIGALG
TGIGGITTSTQPYXKLSGLMGDMERVADSLYTLQDQLNSLAAVVLQNRRALDLLTAE
RGGTCLPLGSECCYYNGSGINGDMERVADSLYTLQDQLNSLAAVVLQNRRALDLLTAE
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/product="envelope glycoprotein"
/protein_id="AAQ17565.1"
/db_xref="G1:33410941"
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84. .1900
note="syncytin"
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/note="splice acceptor site"
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/isolate="individual 148 /
/db_xref="taxon:9606"
/chromosome="7"
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'note="Caucasian
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1 (bases 1 to 2694)
Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G.,
Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
The endogenous retroviral locus ERVWEI is a bona fide gene involve in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
14757826
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Pred. No. 9.2e-304;
0; Mismatches 112;
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                                                                                                     /mol_type="genomic_DNA"
/isolate="individual_22 allele B"
/isolate="individual_22 allele B"
/db_xrexon:9606"
/chromosome="7"
/map="721-q22"
/sex="male"
/cell_type="PBMC's"
/note="Caucasian
endogenous_virus: HERV-W"
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              Lyon 69364 cedex 07, France
Location/Qualifiers
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/organism="Homo sapiens"
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/note="splice acceptor site"
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Bukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 2694)
Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWE1 is a bona fide gene involved
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             Mallet,F., Bouton,O. and Ollet.

Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CRRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69164 cedex 07, France
Location/Qualifiers
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/mate"female"
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endogenous_virus: HERV-W"
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Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMeritux, Ecole Normale Superieure de Lyon - 46 allee
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Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Lvgplvsnlbithtghtcykrsnttythgclirmypppqlyclbggippvcgtsa
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                                                                                                 Mallet, F., Bouton, O. and Oxiol, G.
Mallet, F., Bouton, O. and Oxiol, G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMeritux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69346 cedex 07, France
Location/Qualifiers
Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G., Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWEl is a bona fide gene in howinoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2694)
Mallet, P., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G.,
Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
The endogenous retroviral locus ERVWE1 is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Pred. No. 9.2e-304;
0; Mismatches 112; Indels 13; Gaps
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- 46 allee
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Direct Submission
Submitted (OrJUN-2002) Retrovirology Department,
CNRS-blowerieux, Ecole Normale Superieure de Lyon
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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Best Local Similarity 90.1%;
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Run on:

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Jolivet-Reynaud C, Mandrand
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ADE09587
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AAK04516
ABS29670
AAI04422
ABS04589
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Komurian-Pradel F,
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Adb84403 MSRV-1 as Ab161744 Colon ade Adf59718 Human con Abn97929 Human con Acn44454 Human gen Aaa68626 DNA encod Acas1002 Human dia Aaa63826 Nucleotid Aa41225 Human dia Acc46747 Human dit
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                                                                                                                            1 tcaaaatcgaagagctttag.......gcaaggatcccccagtaaca 1329
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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New nucleic acid from retroviruses - useful for diagnosis, prevention and

WPI; 1998-322732/28. P-PSDB; AAW71069.

Adc38776 Human cDN Aax77526 Human sec Aaz59468 Human sec

Aad24195 Human syn Aaf55630 Nucleotid Aas84210 DNA encod

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Multiple sclerosis; virus; diagnosis; prophylaxis; therapy; expression; rheumatoid polyarthritis; 88.
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                                                                                             Nucleic acid sequences of retrovirus called MSRV-1 - associated with multiple sclerosis or rheumatoid polyarthritis.
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P-PSDB; AAW99554.
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                                                The present sequence represents a multiple sclerosis (MS) associated retrovirus (MSRV) genomic fragment used in the method of the invention. The invention provides complete or partial genomic sequences of the MSRV-genes, gag gene and env gene, and polypeptides encoded by these polypeptides. The invention also provides antibodies raised against the polypeptides. The genomic sequences, polypeptides and antibodies are also claimed useful for diagnosing infection by MS and rheumatoid arthritisassociated viruses, and also for prevention and treatment of infection with these viruses
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100.0%; Pred. No. 0;
ive 0; Mismatches
                                  Disclosure; Page 187-188; 286pp; English
             of, e.g. multiple sclerosis.
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, Jolivet-Reynaud C, Mandrand
                           CTCAAGCTGAGCTTTGTTCGCCATCCACCACTGCTGTT
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                        This sequence represents clone 5M6 from a novel multiple sclerosis related virus type 1 (MSRVI). The sequence can be used in diagnostic, prophylactic or therapeutic compositions to inhibit expression of a multiple sclerosis related virus and/or virus associated with rheumatoid polyarthritis. (Updated on 27-ANG-2003 to correct OS field.) (Updated on 17-OCT-2003 to standardise OS field)
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       Page 39-40; 83pp; French.
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Best Local Similarity
Matches 1329; Conserv
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New isolated or purified nucleic acid associated with multiple sclerosis and/or rheumatoid arthritis, useful for detecting a virus associated with multiple sclerosis or rheumatoid arthritis in a biological sample.
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                                                  GCTGACTTCCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTCTGATCCAGCGAGGT
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Jolivet-Reynaud C, Mandrand
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KOMURIAN-PRADEL F.
JOLIVET-REYNAUD C.
MANDRAND B.
GARSON J. A.
TUKE P W.
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Komurian-Pradel F,
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BESEME F.
BEDIN F.
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 arthritis. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating multiple sclerosis and/or rheumatoid arthris. The present sequence is used in the exemplification of the invention.
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                                                                                                         Query Match

99.8%; Score 1326; DB 12; Length 1329;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1329; Conservative 0; Mismatches 0; Indels 0;
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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                      The invention relates to an isolated or purified nucleic acid from a virus associated with multiple sclerosis and/or rheumatoid arthritis, virus associated with multiple sclerosis and/or rheumatoid arthritis, comultiple sclerosis-associated virus (MSRV)-1. The nucleic acids comprise proteins or defined peptides (including immunodominant peptides, conserved motifs). Also included are a process for detecting a virus associated with multiple sclerosis or rheumatoid arthritis, a correst associated with multiple sclerosis or rheumatoid arthritis, a primer for the amplification by polymerisation of a nucleic acid of a virus associated with multiple sclerosis or rheumatoid arthritis, a properties and a nucleic acid probe for the detection of a virus associated with multiple sclerosis or rheumatoid arthritis, a polypeptide exhibiting an inhibitory activity on the correctly; a polypeptide exhibiting an inhibitory activity from MSRV, and an antibody directed against the MSRV-1 virus obtained by immunologically reacting a human or animal body or cells with an immunologically reacting a human or animal body or cells with an exposure to a virus associated with multiple sclerosis or rheumatoid arthritis or for the nucleic acids are useful for detecting a biological sample, the presence of or exposure to a virus associated with multiple sclerosis or rheumatoid arthritis. The present caseduced with multiple sclerosis or rheumatoid arthritis. The present consisting of the patent do not match the SEQ ID numbers in the sequence listing. Consequences mentioned in the case and the sequences the authors intended to claim.
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The present invention describes a method (M1) for screening for an antineoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in activity and can be used to must ineoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
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prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous call carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour
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                                                                                                         77.9%; Score 1035.2; DB 6; Length 56093; 90.1%; Pred. No. 0; ive 0; Mismatches 111; Indels 13;
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                                                                                                                                                                                                                                                                                                                  The present invention describes isolated polynucleotide sequences (I), which encode polypeptides (II) with biological activity. Also described: (I1) a vector comprising (I); (2) an expression vector comprising (I); (3) a host cell genetically engineered to comprise (I) which is operatively associated with a regulatory sequence that modulates expression of (I) in the host cell; (4) a polypeptide (II) encoded by (I); (5) a composition comprising the polypeptide of (4) and a carrier; (6) an antibody directed against the polypeptide of (4) and a carrier; (6) an antibody directed against the polypeptide of (4); (7) detecting (I) or the polypeptide of (4) in a sample; (8) identifying a compound that binds to the polypeptide of (4); (7) detecting (I) or the polypeptide of (4); (7) detecting (I) or the polypeptide of (4); (7) detecting (I) or the polypeptide of (9) producing the polypeptide of (4); and the polynucleotides sequences (I). The polynucleotides (I) can be used as hybridisation probes, oligomers or primers, for chromosome or gene mapping, for the recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       '; genetic engineering; hybridisation probe; oligomer; mapping; gene mapping; recombinant protein production;
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  proteins, and for generating antisense DNA or RNA. The nce represents a human contig polynucleotide sequence, which
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                                                                                                                                                                                                Gaps
or RNA.
                                                                                                                                             Length 9502;
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                                                                                                 BP; 2813 A; 2433 C; 1992 G; 2263 T; 0 U; 1 Other;
                                                                                                                                                                                           0; Mismatches 129; Indels
                                                                                                                                               DB 10;
                    present sequence represents a human contig polymis used in an example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to new nucleic acid sequences of human endogenouse retrovirus, HERV-7q, which is located on chromosome 7q. Sequiacory elements associated with HERV-7q may alter expression of other genes (even remote genes) on the same chromosome, inducing immunological and/or neurological changes (which may be pathological or protective/curative). HERV-7q peptides can be used to improve efficiency of the immunotherapy. HERV-7q peptides and their coding sequences can be used in immunogenic or vaccinating compositions, for
                                                                             recadedaadedececearrecegerecedareddecraaadderrecearrerecedec 3632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid sequences of human endogenous retrovirus, HERV-7g, used diagnosis, treatment and prevention of autoimmune and neurological
                            GCAGACCTGCCACTGACTTCCATCCCTCTGGATCCTGCAGGTGTCCGCTGTGCTGA
                                                                                                   GGCTAAGTGCCTGGGTTTGTCCTAATAGAACTGAACACTGGTCACTGGGTTCCATGGTTC
                                                                                                                                               TCTTCCATGACCCACGCCTTCTAATAGAGCTATAACACTCACCGCATGGCCCAAGATTCC
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multiple sclerosis; ds.
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protection against autoimmune diseases, particularly multiple sclerosis. The peptides may also be used (by sequence comparison) to detect/identify endogenous retroviruses that are abnormally expressed in cancer, neuropathologies or other autoimmune diseases. The present sequence was used to illustrate the invention
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                                                                                                                                                             TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTT
                                                                                                      77.0%; Score 1023.2; DB 3; Length 10499; 90.1%; Pred. No. 0;
                                                                                  Other;
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0; Mismatches
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Best Local Similarity
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Matches 1132;
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                                                                                                                                                                                                              .0025 ACCCATTGCCGCTCCCAATCGGGCTAAAGGCTTGCCATTGTTCCTGCCATGGCTAAGTGCC
                               GCTGACTTCCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGTCCTGATCCAGCGAGGT
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                                                                                                                                                                                                                                                                                                                                                            1, chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder;
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involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences
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                                                                                                                          TTTTGGTAGCGCCCACCACCATCTTGGGAGCTGTGGGAGCAAGGATCCCCCAGTAACA 1329
                                                                                                                                            CAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAAAATCTACCGTGGACCC 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of bioactive agent capable of bioactive agent capable of modulating the activity of CAP; (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vii) for diagnosing carcinoma; (vii) for neutralizing the effect of CAP; (vii) for treating (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent useful for which no sequence data was published
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                      4330 TAACAGAGCTATAACACTCACCGCATGGCCCAAGGTTCCGTTCTTGTAATCCGTGAGGC
                                                                                 CAAGAACCCCAGGTCAGAGAACAAAAGGCTTGCCACCATCTTGGAAGCGGCCTGCTACCG
                                                             CAAGAACCCCAGGTCAGAGAANGTGAGGCTTGCCACCATTTGGGAAGTGGCCCACTGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21646 BP; 5145 A; 5617 C; 5218 G; 5646 T; 0 U; 20 Other;
                                                                                                                                                                                                                                                                                                                                                              Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 910; Opp; English.
                                                                                                                                                                                                                                                                                                                               Human genomic sequence hCG1748307
                                                                                                                                                                                                                                   ВР
                                                                                                                                                                                                                                   ACN44454 Btandard; DNA; 21646
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The invention relates to polynucleotides (I) encoding diagnostic and therapeutic (DITHP) polypeptides (II), which include e.g. enzymes, and proteins involved in growth and development and receptors. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate DITHP expression. For example, (I) and (I may be used to treat disorders associated with decreased polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                             (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen A, D'sa SA, Amshey
Flores V, Fong WT, Gree
Roseberry AM, Rosen BH,
Wright RJ, Yap PE, Yu,
Cohen HJ, Hodgson DM, 1
                                                       respiratory disorder; ss
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24-FEB-2000;
12-MAY-2000;
15-MAY-2000;
16-MAY-2000;
                                                                                                                     21-FEB-2001;
                                                                      Homo sapiens
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17-MAY-2000;
                                                                                                      30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                              Panzer SR,
                Human
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cc expression by rectifying mutations or deletions in a patient's genome, that affect the activity of the DITHPS, by expressing inactive proteins or supplementing the patient's own production of them. (I) and (II) may be used to treat disease, for example, call proliferative disorder. Crohn's disease, acquired immune deficiency syndrome (AIDS) lymphoma, clenkaemia, autofimmune deficiency syndrome (AIDS) lymphoma, complementary sequences may respiratory disorders. Additionally, complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in camples, and therefore which patients may be in need of restorative camples, and therefore which patients may be in need of restorative camples, and therefore which patients may be in need of restorative camples against DITHPs and in assays to identify modulators of DITHP capression and activity. The anti-DITHP antibodies and antagonists may also be used as diagnostic agenty for detecting the anti-DITHPs in samples (e.g. by enzyme linked immunosorbant assay complements). AASINDS repression human diagnostic and therapeutic 302 GAAGCTGTAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAAA 361 61 Archaccacadaccccredaccedecrecradeceardeacedaritaardararean 120 AGCACTCC-CCCAAGGAAATTTCAACTGCACAACCCCTACTACACCCCCAATTCAGCAGGA 179 362 ATCTACCGTGGACCCGGCCTGCTAGACTATGCTCTGATGTTAATGACATTGAA 421 GAAGCTGTAAAACTACTATTGTTCTTCAAAAGGAGCCCCAGATGCAGTCCATGACTAAG 60 rerracectrireacticacciricecrececerecaceaciacierriecececearea AGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTCCTGTTGAGAG GGTGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCTA 240 CGGGGACTGAGAGACAGAGCTGGATTTCCTAGGCTGACTAAGAATCCCTAAGCCTA NCTGGGAAGGTGACCGCATCCTTTAAACATGGGGCTTGCAACTTAGCTCACACCCGA CCAATC-----AGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAG CAATAGCCAATCATCTATTGCCTGAGAGCACAGCGGGAAGGACAAGGATTGGGATATAAA CTCAGGCATTCAAGCCAGCAACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGC TCTGTTTTCACTCTATTTCACTCTTAAATCATGCAACTGCACTCTTCTGGTCGTTTT |||||| |TCTGT------TTTCACTCTATTAAATCTTGCAACTGCACTCTTCTGGTCTGTGTT TITIATGGCTCAAGCTGAGCTTTTTGTTCGCCATCCACCACTGCTGTTTGCCACCGTCACA GTCACCCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTACTACACTCCAATTCAGTAGGA 21; DB 4; Length 1393; Sequence 1393 BP; 375 A; 352 C; 304 G; 360 T; 0 U; 2 Other; Indels Score 778.8; DB 4; Pred. No. 1.2e-244; 0; Mismatches 112; (DITHP) polynucleotides of the invention 58.6%; Matches 904; Conservative Local Similarity **893 773 713 н 422 121 180 542 602 300 662 360 420 480 833 540 482 Query Match g අ _ැර g \$ g ò 원 ð ò 셤 g ઠે 엄 g ò 셤 à ò ò ઠે ठ R, Spiro PA, Banville SC, Shah P, Chalup MS, Chang SC; D'sa SA, Amshey S, Dahl CR, Dam TC, Daniels SE, Dufour GB; Prong WT, Greenawalt LB, Hillman JL, Jones AL, Liu TF; Y AM, Rosen BH, Russo FD, Stockdreher TK, Daffo A; J, Yap PB, Yu JY, Bradley DL, Bratcher SR, Chen W; Hodgson DM, Lincoln SE, Jackson S; Polynucleotides encoding diagnostic and therapeutic proteins, e.g. erzymes, hormones and receptors, useful in diagnostics and therapeutics Human; receptor; diagnostic; therapeutic; gene therapy; vaccine; cell proliferative disorder; Crohn's disease; lymphoma; leukaemia; acquired immune deficiency syndrome; AIDS; autoimmune disorder; diagnostic and therapeutic polynucleotide (DITHP) #17. Claim 1; Page 304; 522pp; English 2000US-0185216P 2000US-0203785P 2000US-0204226P 2000US-0204821P 2000US-0204801P 2000US-0204801P 2000US-0204815P 2000US-0204815P 2000US-0205281P 2000US-0205281P 2000US-0205281P 2000US-0184768P. 2000US-018470P. 2000US-0184771P. 2000US-0184771P. 2000US-0184772P. 2000US-0184774P. 2000US-0184776P. 2000US-0184777P. 2000US-0184797P. 2000US-0184813P. 2000US-0184837P. 2000US-0184841P. 2000US-0185213P. 2000US-0205287P. 2000US-0205323P. (first entry)

GACCCGCTGCTGCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCC 1012

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(II)

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The present sequence represents the nucleotide sequence corresponding to the 3' env region and long terminal repeat sequences from clone CL6 of Multiple Sclerosis retrovirus (MSRV-1). The specification describes a long terminal repeat (LTR)-RUS region which encodes the expression of a MSRV-1 protein. This is unusual for LTRs, in particular in the RUS region. The sequence includes CAAT and TATA signals which are present in the U3 and R regions and are not directed towards the CDS indicated in the features table. Probes and antibodies to the MSRV-1 retrovirus protein and encoding polymucleotide sequences are used to detect the presence of MSRV-1 retrovirus in a biological sample. (Updated on 06-AUG-2003 to correct OS field.)
to detect the presence of MSRV-1 retrovirus in a biological
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Pred. No. 2.1e-243;
0; Mismatches 63;
                                        English.
                                                                                                                                                                                                                               Sequence 2030 BP; 574 A; 559
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Matches 812; Conservative
                                        Disclosure; Fig 2; 23pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       region; long terminal repeat; LTR; RU5 region; retrovirus;
                                        TAAGTGCCCGGGTTCATCCTAATCGAGCTGAACACTAGTCGCTGGGTTCCACGATTCTCT
                                                                                                                         TCCATGACCCACGGCTTCTAATAGAGCTATAACACTCACCGCATGGCCCAAGATTCCATT
                                                                                                                                        CCTTGGTATCTGTGAGGCCAAGAACCCCAGGTCAGAGAANGTGAGGCTTGCCACCATTTG
                                                                                                                                                                                            Nucleotide sequence of the MSRV-1 3' env and LTR regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                one termination codon"
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                                                                                                                                                                              1503 TGAAGCTGTAAAGCTACAAATGGTTCTTCAAATGGAGCCCCCAGATGCAGTCCATGACTAA
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                                                                          CCTCAGCCAATGGATGCCCTGGACTCCCCTTCTTAGGACCTCTAGCAGCTATAATAT
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                                                                                                   Human, embryogenesis associated protein, AIDS, reproductive disorder; infertility, endometriosis, endometrial tumour, inflammatory disorder; autoimmune disorder, acquired immune deficiency syndrom,; transgenic; ovarian tumour, contact dermatitis, placenta disorder; preeclampsia,
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Pred. No. 1.4e-240;
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Matches 812; Conservative
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Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polypeptide encoded by human diagnostic and therapeutic polynucleotide, and to induce antibodies.
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Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
                                                             28-MAR-2001; 2001US-0279619P.
29-MAR-2001; 2001US-0280067P.
29-MAY-2001; 2001US-0291280P.
17-MAY-2001; 2001US-0291829P.
17-MAY-2001; 2001US-0291849P.
19-JUN-2001; 2001US-0299428P.
20-JUN-2001; 2001US-0299428P.
                                             27-MAR-2002; 2002WO-US010056
                                                                                                                                                          (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                    WPI; 2003-129518/12.
                                                                                                                                                                                                                                              P-PSDB; ABR41810
        WO200297031-A2
                           05-DEC-2002
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The invention relates to novel human diagnostic and therapeutic polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded proteins (DITHP; ABR41186-ABR41812). The invention also relates to polynucleotide sequences at least 90% identical to the dithp CDNA sequences of the invention; recombinant vectors, host cells and recombinant production of DITHP proteins; antibodies specific for DITHP croceins antibodies specific for DITHP proteins; antibodies specific for DITHP proteins; antibodies specific for DITHP proteins antibodies specific for DITHP correcting dithp nucleotide and protein sequences; methods of detecting dithp nucleotide and protein sequences; methods of casessing the toxicity of test compounds using a dithp hybridisation probe. Dithp nucleic acid sequences and DITHP proteins and other cell casessing the toxicity of fconditions including cancer and other cell contains of a wide variety of conditions including cancer and other cell croceins and connective tissue disorders; neurological disorders; pastrointesfinal disorders; metabolic disorders; neurological disorders; pastrointesfinal disorders; transport concerns can additionally be used in analysis of the proteome of a tissue or cell type and to induce antibodies. They may also be used to sortein can additionally useful in somatic or germline gene therapy of the disorders additionally useful in somatic or germline gene therapy of the disorders additionally useful in somatic or germline gene therapy of the disorders concent and to induce antibodies. They may also be used to the protein additionally useful in somatic or germline gene therapy of the disorders and additionally useful in somatic or germline gene therapy of the disorders and primers, in genotyping and identification of individuals, in toxicological testing, and in transcript imaging. The present sequence represents a dith provent and expected or this patent did not form part of the presence sequence fo ftp.wipo.int/pub/published_pct_sequences Claim 2; SEQ ID NO 668; 591pp; English.

Sequence 2046 BP; 587 A; 494 C; 391 G; 566 T; 0 U; 8 Other;

257 CCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAATTGAAGCTGTAAAGCTA 316 Query Match

56.3%; Score 747.6; DB 8; Length 2046;
Best Local Similarity 86.5%; Pred. No. 2.9e-234;
Matches 885; Conservative 0; Mismatches 122; Indels 16;

1154 1111 caacccccrtrgggrccccrcccrrrgrarggagcrcrgr-----rrrcacrcr 1160 977 TTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGCGAGGTACCCATTGCCACTCCC 1036 GATCAGGCTAAAGGCTTGCCATGTTCCTGCATGGCTAAGTGCCTGGGTTTGTCCTAATA 1096 1215 AA-CCCCAGGTCAGAGAANGTGAGGCTTGCCACCATTTGGGAAGTGGCCCACTGCCATTT 1273 AACCCCCAGGTCAGAGAACACGAGGCTTGCCATCATCTTGGAAGTGGCCCCACGACCATC 1577 916 976 736 930 676 436 496 CICIGIAICITIAACCICCIIGIIAAGIIIGICICITICCAGAAIIGAAACIGIAAAACIA 630 AGAGCTATAACACTCACCGCATGGCCCAAGATTCCATTCCTTGGTATCTGTGAGGCCAAG 1221 detriceagrecacederedrearegregereteredadecededegeredeceeer 1097 GAACTGAACACTGGTCACTGGGTTCCATGGTTCTCTT-CCATGACCCACGGC-TTCTAAT AGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCTANCTGGGAAGGTGACC 617 GCATCCATCTTTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC ACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCCAATCATTGCCTG ATTAAATCATGCAACTGCACTCTTCTGGTCCGTGTTTTTTATGGCTCAAGCTGAGCTTTTTTT TGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTCCTGTTGAGAGGGTGGACTGAGAGAC GITCGCCATCCACCACTGCTGTTTGCCACCGTCACAGACCCGCTGCTGACTTCCATCCCT CTGGACCGGCCTGCTAGACTATGCTCTGATGTTAATGACATTGAAGTCACCCCTCCCGAG CAACCCCCTTTGGGTCCCCTTCCCATTGTATGGGAGCTCTGTTTTCACTCTTTCACTCT CAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAAAATCTACCGTGGACCC GAAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGGAAGCAGTTAGAGCAGT TGG 1276 917 1155 1274 677 197 857 1037 1461 1518 497 557 571 317 631 377 691 437 요 Q g g g g ò g 셤 ò g ò g ò ò ð 셤 ò Š ò ò 8 a ò 셤 ò g g ò ઠે

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2775 AATCATCTATTGCCTGAGAGCACAGGAGGAGGAGAATGATCGGGATATAAACCCAAGTC
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              CCTCAGCCAATGGATGCCCTGGATTCTCCCCTTCTTAGGACCTCTAGCAGCTATAAATATT
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                                                         241 TITACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAAT
                                                                                                                                                                                  361 AATCTACCGTGGACCCCTGGACCGGCCTGCTAGACTATGCTCTGATGTTAATGACATTGA
                                                                                                                                                                                                                                                                                                             481 AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGGTTTTCCTGTTGAGA
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                                                                                                                        Secreted protein; testes; brain; blood; placenta; human; murine; thymus; bone marrow; treatment; prevention; nutrition; cytokine; immune; vaccine; cell proliferation; cell differentiation; suppressor; tumour inhibition; haematopoiesis regulator; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; receptor; ligand; anti-inflammatory; tumour; cadherin; tumour invasion suppressor; gene therapy; tissue growth; ss.
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Pred. No. 5.7e-229;
0; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides encoding secreted proteins
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 BP.
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                                                                                              Human secreted protein AJ172_2
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98US-00080478.
98US-00175928.
 standard; cDNA; 2946
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Treacy M;
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20-OCT-1998;
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Merberg D,
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                                                                                                                                                                                                                                                                                                                                                                                                                         2835 TricgAgccagcAAcccccrrrrdGGrccccrcccrrrGrArGGAGCrcrrrr 2894
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                                                              GGGTGGACTGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCT
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96US-00721926.
96US-00738367.
96US-00739775.
97US-00783395.
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96US-00664596.
96US-00677231.
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96US-00721798
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96US-00635311
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09-JUL-1996;
26-JUL-1996;
23-AUG-1996;
27-SEP-1996;
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19-APR-1996;
07-JUN-1996;
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10-APR-1997;
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                                                                                                                                                                                                                                                                                                                           This is the human secreted protein AJ172 2 nucleotide sequence, obtained from a human adult testes CDNA library. The invention relates to secreted human and murine proteins. The polymucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Detecrion of the levels of the proteins can be used for the diagnosis of e.g. pre-eclampsia, placental pathology or cancer. Agents which modulate the expression or function of the proteins may be used for treating a neoplastic disease and inhibiting metastasis. Other suggested activities include nutritional activity (e.g. in feeds), cytokine and cativities include nutritional activity (e.g. in feeds) cytokine and cativity, expression activity, immune stimulating (e.g. as vaccines) or suppressing activity, haemostatic and thrombolytic activity, themostatic activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, creeptor/ligand activity, and tumour inhibition activity. The invasion suppressor activity, and tumour inhibition activity. The propressor activity, and tumour inhibition activity. The propression are also stated to be useful for gene therapy
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                                                                                                                                                                                                                               New polynuclectides encoding secreted cDNA libraries, used to develop products for the diagnosis and treatment of neoplastic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                              Evans C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2946 BP; 858 A; 801 C; 570 G; 717 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69; Indels
                                                                                                              Collins-Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 731.8; DB 3;
Pred. No. 5.7e-229;
0; Mismatches 69;
                                                                                                                                                                                                                                                                                              Claim 14; Page 107-108; 149pp; English.
                                                                                                            Lavallie ER,
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90.7%;
              98US-00080478.
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                                                                       GEMY ) GENETICS INST INC.
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Best Local Similarity 90.7
Watches 794; Conservative
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                                                                                                                                                                         2000-116311/10.
                                                                                                                Mccoy J
Mi S,
                                                                                                                                                                                           P-PSDB; AAY67313
              18-MAY-1998;
20-OCT-1998;
                                                                                                                Jacobs K,
Merberg D,
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2775 AATCATCTATTGCCTGAGAGCACAGGAGGGACAATGATGGTCGGGATATAAACCCAAGTC 2834
2415 GAICTACCGCAGACCCCTGGACCGGCCTGCTAGCCCACGATCTGATGTTAATGACATCAA 2474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     721 AATCATCTATTGCCTGAGAGGACAGGGAAGGACAAGGATTGGGATATAAACTCAGGCA 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2835 TTCGAGCCGGCAACGCCAATGGGTCCCCTCCCTTTGTATGGGAGCTCTGTTT
                                                                                                                                                                                                                                                                                                                                  TTCAAGCCAGCAACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTT
                                                                                    2475 AGGCACCCCTCCTGAGGAAATCTCAGCTGCACAACCTCTACTACGACCCCCAATTCAGCAGG
                                                                                                                                                                                  2535 AAGCAGTTAGAGCGGTCGTCGGCCAACCTCCCCAACACAGCACTTAGGTTTTCCTGTTGAGA
                                                                                                                                                                                                                            541 GGGTGGACTGAGGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCT
                                                                                                                                                                                                                                                                                                          ANCTEGGAAGGTGACCECATCCATCTTTAAACATGGGGCTTGCAACTTAGCTCACACCCG
                                                             agicaccccccccccaagaaaicicaacigcacaacccctactacactccaaitcagiagg
                                                                                                                                             AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTCCTGTTGAGA
                                                                                                                                                                                                                                                   ACCAATCAGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, syncytin; preeclampsia; gestational trophoblast disorder; choriocarcinoma; hydatiform mole; placental site tumour; abortion; envelope gene; human endogenous defective retrovirus; HERV-W; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or at risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying a compound for treating a subject with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACTCTATTTCACTCTATTAAATCATGCAACTGCA 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/product= "Syncytin"
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930. .2546
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JUL-2001; 2001WO-US021719.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-171727/22.
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                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a protein comprising fully defined A2302 1

protein or BD127 16 protein. The polynucleotides are useful for
expressing recombinant proteins for analysis and are also useful as
chromosome markers or tags to identify chromosomes or to map related
continue. The proteins are useful as amino acid supplement, carbon
continue introgen source and carbohydrate source. The proteins are useful
continued immunodeficiency (SCID); autoimmune disorders (e.g. severe
combined immunodeficiency (SCID); autoimmune disorders (e.g. multiple
combined immunodeficiency (SCID); autoimmune disorders (e.g. multiple
combined immunodeficiency (SCID); autoimmune disorders (e.g. multiple
compined is systemic lupus errythematosus, rheumatoid arthritis), allergic
reactions (e.g. asthma), myeloid or lymphoid cell deficiencies,
coteoporosis or osteoarthritis, peripheral nervous system diseases (e.g.
peripheral neuropathy, Alzheimer's disease, Parkinson's disease),
coagulation disorders, inflammatory diseases (e.g. systemic inflammatory
cresponse syndrome (SIRS), ischaemia-repertusion injury, Crohn's disease),
coagulation minounity, for inducing pone, cartilage, tendon, ligament and/or
nerve growth or regeneration, for proliferating neural cells and for
cuestul as inhibitors of receptor/ligand interactions. The present
constitution and interactions are also useful for
mammalian cells (e.g., monocytes, fibroblasts, neutrophils), and also
cuestul as inhibitors of receptor/ligand interactions. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proteins AZ3021 encoded by clone AZ3021 from human adult colon, and BD12716 encoded by clone BD12716 from human fetal kidney cDNA library, useful for treating e.g. multiple sclerosis and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTAATTTT
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Best Local Similarity 90.7%; Pred. No. 5.7e-229;
Matches 794; Conservative 0; Mismatches 69; Indels 12;
                                                                                                                                         Collins-Racie LA, Evans C;
Spaulding V, Carlin-Duckett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence represents cDNA encoding a human secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2946 BP; 858 A; 801 C; 570 G; 717 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 134; 412pp; English
                                                                                                                                           Lavallie ER,
                                                                                                                                                                 Bowman MR,
                   97US-00867677.
97US-00924838.
99US-00413232.
                                                                                                       (GEMY ) GENETICS INST INC.
                                                                                                                                                                 Treacy M,
                                                                                                                                         Jacobs K, Mccoy JM,
Merberg D, Treacy M,
Kelleher K;
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P-PSDB; ADC38777.
                       02-JUN-1997;
05-SEP-1997;
06-OCT-1999;
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protein. The specification describes a method for detecting expression of an envelope protein from a human endogenous retrovirus (HERV), in cells, of a tissue or culture. The method comprises detecting syncytia formation due to the fusogenic properties of the envelope protein. Envelope plypaptides and polymucleotides are used to produce therapeutic or prophylactic compositions, particularly for treatment of cancer, to correct defects in placental development (or other natural formation of other types of syncytia), and to promote adhesion of cells in grafts or cellular repair processes. Expression of sequences antisense to the polymucleotide are used to prewent formation of syncytia
2777 AATCATCTATTGCCTGAGAGCACAGGAGGGACAATGATCGGGATATAAACCCAAGTC 2836
                                                                       tricasacidedesaceschareceertrieserecerecerrieraressagerereriri 2896
                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of a human endogenous retrovirus envelope protein.
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                                                                                                                                                                                                                                                                                                                                                                                                   Envelope protein; HERV; syncytia formation; placental development;
syncytia; cancer; cell adhesion; 8s.
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                                                                                                                                       CATGCTATTTCACTCTATTAAATCTTGCAACTGC 2930
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/product= "envelope protein"
                                                                                                                   CACTCTATTTCACTCTATTAAATCATGCAACTGC
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(INRM ) INST NAT SANTE & RECH MEDICALE.
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99FR-00011793
                                                                                                                                                                                                                                                    AAF55630 standard; DNA; 2781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human endogenous retrovirus.
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P-PSDB; AAB67652.
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Matches 793; Conserv
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                                                                                                                   The invention relates to identifying compounds which are modulators of syncytin expression. The syncytin modulators are useful in diagnosis and treatment of preeclampsia and gestational trophoblast disorders (e.g. choriocarcinoma, hydatiform mole, placental site tumour and missed/incomplete abortion). Syncytin is a human gene derived from the envelope gene of human endogenous defective retrovirus, HRRV-W. The present invention is based partly on the discovery that syncytin expression is dramatically reduced in preeclampsia, and is also mis-localised to the apical syncytiotrophoblast membrane. The present sequence is human
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         developing preeclampsia, comprises determining whether the expression or activity of syncytin in the cell is modulated in the presence of a test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGGGAAGAATGCTGTTAGTATGTTAATCAATCTGGAATCATTACTGAGAAGTTAAAGA
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Pred. No. 1.2e-228;
                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                     Disclosure; Page 39-42; 43pp; English.
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Best Local Similarity 90.7%;
Matches 793; Conservative
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 20014; 103pp; English
                                                                           31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                    30-MAR-2001; 2001WO-US008631
                                                                                                                                                           2001-639362/73
                                                                                                               (HYSE-) HYSEQ INC
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          WO200175067-A2.
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                                                                   AATTTGAGATCGAATATAATGTAGAGCAGGACCTTCAAAACACTGCACCCTGGGGCCT
                                                                                         AATTCGAGATCGAATACAACGTAGAGCAGGAGCTTCGAAACACTGGACCCTGGGGCCT
                                                                                                                CCTCAGCCAATGGATGCCCTGGACTCTCCCCTTCTTAGGACCTCTAGCAGCTATAATATT
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed control useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food of sites expressing (II). (II) and (II) are useful in medical imaging of sites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The colypeptide and polymucleotide sequences have applications in a polymoral control contr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6394 BP; 1840 A; 1597 C; 1384 G; 1571 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 6394;
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Pred. No. 1e-227;
0; Mismatches 223;
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78.6%;
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Best Local Similarity 78.6
Matches 1094; Conservative
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Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss. novel human diagnostic protein #20014.

(first entry)

13-FEB-2002

AAS84210;

DNA encoding

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This sequence represents the complete sequence of the human endogenous retrovirus (HERV) W genome. The nucleic acids, their fragments or peptides encoded by them are markers of autoimmune disease (e.g. multiple sclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulin- dependent diabetes and related pathologies) and of abnormal or susceptibility to these conditions, or proximity markers for sescotiated with this susceptibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTACTCCTCTTTGGACCCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTTTCCAGAAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid sequences from human endogenous retrovirus-W - expressed exclusively in placenta and useful in diagnosis and therapy of autoimmune disease, and abnormal or failed pregnancy.
                                                                                                                                                                                                                                                                                               Clone; human endogenous retrovirus; genome; autoimmune disease; multiple sclerosis; rheumatoid polyarthritis; insulin-dependent diabetes; disseminated lupus erythematosus; pregnancy; chromosomal marker; ss.
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..1e-225;
                                                                                                                                                                                                                                                        Complete human endogenous retrovirus W genome
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88.5%; Pred. No. 1.1e
:ive 19; Mismatches
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                                                                                                                 BP,
                                                                                                                 mRNA; 7582
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Matches 774; Conservative
  CCCCGGTAACA 2553
                                                                                                                   AAX25665 standard; cDNA
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                                                                                                                                                               AAX25665;
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AAGGCACCCTCCTGAGGAAATCTCAGCTGCAAAAACCTCTACTTACGCCCCAATTCAGG 1642
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                                                                          AATCTACCGTGGACCCCT-GGACCGGCCTGCTAGACTATGCTCTGATGATGACATTG
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                                                                                                      AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTCCTTGAGA
                                                                                                                       AAGCAGTTAGAGCGGTSGTCGGCCAACCCCCAACAGCACTTAGGTTTTCCTGTTGAGA
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                                  AATCTACCGTGGACCCCTGGACCGGCCTGCTAGACTATGCTCTGATGACATTGA
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The present sequence represents an endogenetic retrovirus, which is associated with an autoimmune disease, and is integrated into the human genome. The retrovirus is human endogenous retrovirus W (HERV-W). The HERN-W retrovirus is associated with autoimmune disease, failure of pregnancy of disorders of pregnancy. HERN-W nucleic acid fragments, or proteins derived from it, are useful for diagnosis of autoimmune disease (specifically multiple sclerosis) and for monitoring pregnancy. The nucleic acid fragments may also be used for in situ labelling of isolated chromosomes, while the transcription product can be used to study or monitor I cell proliferation in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 ITTACTCCTCTTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAAT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTCAGCCAATGGATGCCCTGGACTCTCCCCTTAGGACCTCTAGCAGCTATAATATT
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88.5%; Pred. No. 1.1e-225;
rative 19; Mismatches 70;
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                                                                                                                                                               Gaps
(HERV) W genome. The nucleic acids, their fragments or peptides enco by them are markers of autoimmune disease (e.g. multiple aclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulindependent diabetes and related pathologies) and of abnormal or unsuccessful pregnancy and can be used as chromosomal markers for susceptiblity to these conditions, or proximity markers of genes associated with this susceptibility
                                                                                                                                                               12;
                                                                                                                                   Length 1136;
                                                                                                         Sequence 1136 BP; 336 A; 289 C; 241 G; 270 T; 0 U; 0 Other;
                                                                                                                                                               Indels
                                                                                                                                 Score 721.2; DB 2;
Pred. No. 9.9e-226;
0; Mismatches 75;
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Matches 787; Conservative
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194 GCTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAACTTTGTCTCTTCCAGAAT
                                                                                                  361 AATCTACCGTGGACCCCTGGACCGGCCTGCTAGACTATGCTCTGATGTTAATGACATTGA
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                                                                                                                                                                             gene and 3' non coding sequences of HERV-W from human genome
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Best Local Similarity 90.0%; Pred. No. 9.9e-226; Indels 1136; Matches 787; Conservative 0; Mismatches 75; Indels 12;
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                                                                                                                   This sequence represents clone cl.PH74 of the human endogenous retrovirus (HERV) W genome. The nucleic acids, their fragments or peptides encoded by them are markers of autoimmune disease (e.g. multiple sclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulinteumatoid dispetes and related pathologies) and of abnormal or unsuccessful pregnancy and can be used as chromosomal markers for susceptibility to these conditions, or proximity markers of genes
New nucleic acid sequences from human endogenous retrovirus-W - expressed exclusively in placenta and useful in diagnosis and therapy of autoimmune disease, and abnormal or failed pregnancy.
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Pred. No. 1.1e-
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The present sequence represents an endogenetic retroviral nucleic acid fragment, which is associated with an autoimmune disease, and is integrated into the human genome. The fragment is originally derived from a novel retrovirus, human endogenous retrovirus W (HERV-W). The HERV-W retrovirus is associated with autoimmune disease, failure of pregnancy or disorders of pregnancy. The nucleic acid fragment, or proteins derived from it, are useful for diagnosis of autoimmune disease (specifically multiple sclerosis) and for monitoring pregnancy. The nucleic acid fragments may also be used for in situ labelling of isolated chromosomes, while the transcription product can be used to study or monitor T cell
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                               TTCAAGCCAGCAACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and 3' non coding sequences of HERV-W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Autoimmune disease; retrovirus; human endogenous retrovirus W; gag gene; pregnancy; multiple sclerosis; T cell proliferation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human endogenous retrovirus; HERV-W; HERV; chromosome 7; env protein; envelope protein; multiple sclerosis-related superantigen; vaccine; surface antigen; transmembrane; multiple sclerosis; neuroprotective;
                                                                                                                       AATCTACCGTGGACCCTGGACCGGCCTGCTAGACTATGATGACATTGA
                                                                                                                                                                                                AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTCCTGTTGAGA
                                                                                                                                                                                                          GGGTGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCT
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                   2082 CCTCAGCCGATGGATGCCCTGGATTCTCCCCCTTCTTAGGACCTCTAGGAGCTATAATATT
                                             241 TTTACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAAT
         CCTCAGCCAATGGATGCCCTGGACTCTCCCCTTTAGGACCTCTAGCAGCTATATATT
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Con the basis of the PBS t-RNA motif used for the classification of human endogenous retrovirus (HERV8) the full length endogenous provirus which was been located on the long arm of human chromosome 7 (7021-22) has been easignated HERV-W. The present invention describes proteins or peptides (C in having superantigen (SAG) activity comprising the ENV protein (ENV) of HERV-W the surface protein (SU) and transmembrane (TM) sub-units. (I) have nuroprotective activity, and can be used in: vaccines; antisensetherapy; and HERV-W SAG activity-inhibitors. (I) and encoding DNA/RNA are therapy; and HERV-W SAG activity-inhibitors. (I) and encoding DNA/RNA are useful for diagnoshing multiple sclerosis (MS) or HERV-W-wassociated crocovering) capable of binding to a retroviral superantigen associated with MS, substances capable of blocking SAG activity and substances capable of blocking SAG activity and substances capable of blocking capable of generating or transcription or translation of SAG activity and being capable of generating an immune response against HERV-W retroviral SAG activity, capable of blocking transcription or capable of blocking the second with MS, or capable of blocking transcription or capable of blocking transcription or translation of HERV-W retroviral superantigen for use in treating or translation of HERV-W retroviral superantigen for use in treating or prevention of MS. (I) and nucleic acids encoding them are useful for diagnosing autoimmune disease. The present sequence encodes the capablatically claimed envelope protein of HERV-W designated G specifically claimed envelope protein of HERV-W designated G
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Pred. No. 1.1e-222;
0; Mismatches 81; Indels 12;
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| (pos:790. .792, aa:Phe) | (pos:793. .795, aa:Thr) | (pos:812. .814, aa:Leu) | (pos:862. .864, aa:Thr) | (pos:862. .864, aa:Thr) | (pos:865. .867, aa:Gln) | (pos:1903. .1105, aa:Leu) | (pos:2013. .1905, aa:Gln) | (pos:2026. .2028, aa:Leu) | (pos:2026. .2028, aa:Leu) | (pos:2026. .2028, aa:Leu) | (pos:2026. .2028, aa:Leu) | (pos:2026. .2028, aa:Leu) | (pos:2026. .2028, aa:Leu) | (pos:2026. .2028, aa:Leu) | (pos:2026. .2028, aa:Leu) | (pos:2026. .2028, aa:Leu) | (pos:2026. .2028, aa:Leu) | (pos:2026. .2028, aa:Leu) | (pos:2026. .2028, aa:Leu) | (pos:2026. .2028, aa:Leu) | (pos:2089. .2091, aa:Clu) |
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Matches 782; Conservative
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                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                                                                               The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481 AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTCCTGTTGAGA
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Pred. No. 3.3e-220;
0; Mismatches 79;
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                                                                                                                                                                                                                                                                                                                                       Claim 25; SEQ ID NO 4541; 487pp; English
                                                                                                                                                                                                                       Rank DR
                                                            04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0204465F.
30-UJN-2000; 2000US-0060840B.
03-AUG-2000; 2000US-00632366.
21-SEB-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
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89.7%;
                            30-JAN-2001; 2001WO-US000670
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Matches 770; Conservative
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   09-AUG-2001
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scification, but was obtained in electronic format directly ftp.wipo.int/pub/published_pct_sequences
                               0 Other
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Pred. No. 3.3e-220;
0; Mismatches 79;
                             Sequence 1894 BP; 557 A; 500 C; 361 G; 476 T; 0
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89.7%;
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Best Local Similarity 89.7
Matches 770; Conservative
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     GGGTGGACTGAGAGAGAGAGTTGCTAGGCTGACTAAGAATCCCNAAGCCT
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30-UNA-2000; 2000US-0608408.
03-AUG-2000; 2000US-053336.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023459P.
04-OCT-2000; 2000GB-00024263.
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                  AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTTCCTGTTGAGA
AATCTACCGTGGACCCTGGACCGGCCTGCTAGACTATGATGATGACATTGA
                                                             AGTCACCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGG
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26-MAY-2000; 2000US-0207456P.
30-UTN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
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                                                                                 placenta
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                                                                                                       Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder; ss.
                                                                                 used to measure gene expression in human
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0; Mismatches 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene expression in human placenta.
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26-MAY-2000; 2000US-0207456P.
30-UNY-2000; 2000US-05608408.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US000663
                                                     (first entry)
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Matches 770; Conservative
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GAAATAGCCAATCATCTCTTGCCTGACAGCACAGCAGGAGGACAATGATCGGGATATAA 1740
                                                                                                                                                                                                       The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                    772 ACTCAGGCATTCAAGCCAGCAACAGCAACCCCTTTGGGTCCCCTCCCATGTATGGGAG
                                                                                             Probe #4444 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
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                                                                                               The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are proposed for general discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring and expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional nucleic acid probe of the invention. Note: The sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained for interior format directly from WINDO at
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for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
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                                                           Claim 1; SEQ ID NO 4517; 327pp + Sequence Listing; English.
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Pred. No. 3.3e-220
0; Mismatches 79;
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                 Human; bone marrow
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26-MAY-2000; 2
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                                                                 AGGGGAAGAATGCTGTTAGTATGTTAATCTAGTCAATCATTACTGAGAAAGTTAAAGA
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Pred. No. 3.3e-220;
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1021 AGAGGAAAATGCTGTTGTTATGTTAATCCAGAATCATCACCGAGAAAGTTAAAGA 1080
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llarity 89.7%; Pred. No. 3.3e-220;
Conservative 0; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                         Human liver single exon probe, SEQ ID No 4660.
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2000US-0234687P.
2000US-0236359P.
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                                                                                                                                                              standard;
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tes 770; Conserv
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27-SEP-2000;
04-OCT-2000;
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1621 ACCAATCAGATACTAAAGAGGGCTCACTAAAATGCTAATTAGGCAAAAACAGGAGATAAA 1680
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1441 AAGCAGTTAGAGTGGTTGTTGGCCAACCTCCCCAACAGCAGTTGGGTTTTCCTGTTGAGA 1500
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                                                                  601 ANCTGGGAAGGTGACCGCATCCATCTTTAAACATGGGGCTTGCAACTTAGCTCACACCCG
                                                                                                                                                                                                    661 ACCAATC-----AGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAA
                                           GGGTGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon probe from lung SEQ ID No 4580.
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                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and noncarding tumours. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                            measuring gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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Pred. No. 3.3e-220;
0; Mismatches 79; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1894 BP; 557 A; 500 C; 361 G; 476 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                              Novel single exon nucleic acid probe used to
                                                                                                                                                                                                                                                                                                                                                                        Claim 25; SEQ ID NO 4413; 322pp; English.
                                                                                                                                                                                                                               Rank DR
                               04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0204465F.
30-UJN-2000; 2000US-0060840B.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000US-023659P.
                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
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Local Similarity 89.7%;
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived functed acid probes for measuring gene expression in a sample derived from thusan lung comprising single exon nucleic acid probes having one of 15614 nucleic acid sequences mentioned in the specification, or their complements or the 12187 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung, measuring gene expression in a sample collection of detectably labeled nucleic acids derived from human lung collection of detectably labeled nucleic acids derived from human lung areas identifying accors in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably algorithmically predicting at least one exon from genomic sequences of the event and (b) measuring the expression of experising (a) dentifying exons from genomic sequences for the method above mentioned microarray; assigning exons to a single exon probe, the exons should be assigned to a single gene; a peptide comprising one of incorparray having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that consistence and for identifying exons in a gene; a peptide comprising one of incorparay mentioned in the sequences, and for identifying exons in a gene; particularly using human clung derived manh and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary diseases such as asthma, lung cancer, chronic obstructive pulmonary diseases such as asthma, lung cancer, chronic obstructive bulmonary diseases such as astima, lung corposed part of pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO specification, but was obtained in electron: at ftp.wipo.int/pub/published_pct_sequences

Gaps 9; Length 1894; Sequence 1894 BP; 557 A; 500 C; 361 G; 476 T; 0 U; 0 Other; Indels 53.0%; Score 704.8; DB 6; 89.7%; Pred. No. 3.3e-220; iive 0; Mismatches 79; Best Local Similarity 89.7 Matches 770, Conservative Query Match

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The invention relates to isolated polynucleotide (I) and polypeptide (II)

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1501 GGGGGGACTGAGAGAGAGAATAACTAGATTTCCTAGACCAACTAAGAATCCCTAAGACT 1560 099 540 771 1561 AGCTGGGAAGGTGACCGCTTCCACCTTAAACACCGGGCTTGCAACTTAGCTCACGCCA GCAATAGCCAATCATCTATTGCCTGAGAGCACAGGGAAGGACAAGGATTGGGATATAA ANCTGGGAAGGTGACCGCATCCATCTTTAAACATGGGGCTTGCAACTTAGCTCACACCCG ACCAATC-----AGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAA ACTCAGGCATTCAAGCCAGCAACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAG 1441 AAGCAGTTAGAGTGGTTGTTGGCCAACCTCCCCAACAGCAGTTTGGGGTTTTCCTGTTGAGA 541 GGGTGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCT AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTCCTGTTGAGA AGTCACCCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGG Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss. New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess DNA encoding novel human diagnostic protein #13117. Claim 1; SEQ ID NO 13117; 103pp; English 1801 Crcrcrrcrcrcrarr 1818 AAS77313 standard; cDNA; 2942 BP CTCTGTTTTCACTCTATT 849 ĭ, 30-MAR-2001; 2001WO-US008631 31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167. Tang (first entry) WPI; 2001-639362/73. P-PSDB; ABG13126. Drmanac RT, Liu C, (HYSE-) HYSEQ INC. WO200175067-A2 biodiversity. 13-FEB-2002 Homo sapiens. 11-OCT-2001. AAS77313; 601 712 772 832 481 661 421 원 ò g ð d ð 셤 ò 셤 ò 셤 ò g ò 요

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Pred. No. 4e-212;
0; Mismatches 127; Indels
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Matches 863; Conservative (
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1982 TGTCACAGACCCACAGCTGACTTCCATCCCTCTG---
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1031 1091 ñ 549 971 661 721 781 129 911 601 440 500 189 560 249 620 671 731 429 791 489 851 craecregarriccraegeccacraagaarcccraaccraecregaaagaraaccacar 309 polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic options of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences 69 GCCTGAGAGCACAGCGGGAAGGACAAGGATTGGGATATAAACTCAGGCATTCAAGCCAGC AACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTTCACTCTATTTC TCCCTTTGGATCCAGGGGTGTCCACTGTGCTCCTGATCCAGCGAGGTACCCATTGCCA 662 cecerecadararedecadedrefeceraterefeararadeaadegececearrece creccaaregeerraaageeregeearrerrecrecaregeraagreecegerregee AGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCCAATCATCTATT ACTCTATTAAATCATGCAACTCTTCTGGTCCGTGTTTTTTAAATCAAGCTGAG ArcriscaAcreca----cAcrerrersererererrareracesercase CTTTTGTTCGCCATCCACCACTGCTGTTTGCCACCGTCACAGACCCGCTGCTGACTTCCA crircecricaccerceaccacrecrerrreceaccerrecacaccarcecreacre CTCCCGATCAGGCTAAAGGCTTGCCATTGTTCCTGCATGGCTAAGTGCCTGGGTTTGTCC 70 ACCGGCCTGCTAGCCCACGATCTGATGTTAATGACATCAAAGGCACCCCTCGTGAGGAAA 370 AGCCCGCTAAAATGCTAATTAGGCAAAAACAGGAGGTAAAGAAATAGCCAATCATCTATT 321 TAGTICTICAAATGGAACCCCAGATGCAGTCCATGACTAAAATCTACCGTGGACCCCTGG 10 TAAAACTACAAATGGAGCCCAAGATGCAGTCCAAGACTAAGATCTACGAGACCCTGG ACCGGCCTGCTAGACTATGCTCTGATGACATTGAAGTCACCCCTCCCGAGGAAA TCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGGAAGCAGTTAGAGCAGTTGTC rereagerecacaacereracraceceeaarreageaggaagaragagegregre 501 AGCCAACCTCCCCAACAGTACTTGGGTTTTCCTGTTGAGAGGGTGGACTGAGAGACAGGA GGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGATGGGGGACTGAGAGACAGGA CTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCTANCTGGGAAGGTGACCGCAT -----AGAG Gaps 17; Length 893; Seguence 893 BP; 223 A; 264 C; 202 G; 204 T; 0 U; 0 Other; 49.0%; Score 651; DB 5; Length 89 Ilarity 85.0%; Pred. No. 1.1e-202; Conservative 0; Mismatches 117; Indels CCATCTTTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATC-Similarity 757; Query Match Best Local S: Matches 757 490 1032 430 792 550 912 602 972 722 381 250 732 852 130 190 672 441 561 621 g 요 g 셤 셤 g ò ò ò ò ò 유 ò g 셤 ઠે ò ઠે 셤 ò 셤 ò a ò 요 ò õ

The present invention relates to new nucleic acid sequences of human endogenouse retrovirus, HERV-7q, which is located on chromosome 7q. Regulatory elements associated with HERV-7q may alter expression of other genes (even remote genes) on the same chromosome, inducing immunological and/or neurological changes (which may be pathological or protective/curative). HERV-7q peptides can be used to improve efficiency of the immunotherapy. HERV-7q peptides and their coding sequences can be used in immunotherapy. HERV-7q peptides and their coding sequences can be used in immunotherapy. HERV-7q peptides and their coding protection against autoimmune diseases, particularly multiple sclerosis. The peptides may also be used (by sequence comparison) to detect/identify neuropathologies or other autoimmune diseases. The present sequence was New nucleic acid sequences of human endogenous retrovirus, HERV-7q, use for diagnosis, treatment and prevention of autoimmune and neurological 22893 TCAAAATTGAAGAGCTTTAGACTTGCTAACCTCTGAAAGAGGGGGAAGCTGTTATTTT ATCTGGAATCATTACTGAGAAAGTTAAAGAAATTTGAGATCGAATATAAATGTAGAGCAGA TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTT -----TATGTTAATCA Gaps Sequence 46340 BP; 16104 A; 8738 C; 8434 G; 13064 T; 0 U; 0 Other; Length 46340; 46; AATAGAGCTATAACACTCACCGCATGGCCCCAAGATTCCATTCCTTGGTATC Autoimmune disease; HERV-7q; chromosome 7q; immunotherapy; Indels Score 643.4; DB 3; Pred. No. 3.6e-199; 88; RECH MEDICALE. 0; Mismatches Claim 15; Page 186-199; 225pp; French. AGGGGAAGAATGCTGTTAG---to illustrate the invention BP. SANTE & ABN97978 standard; DNA; 46340 Rieger 48.4%; 99WO-FR001513 98FR-00007920 Human endogenous retrovirus. 01-AUG-2002 (first entry) Human retroviral sequence Query Match
Best Local Similarity 85.4
Matches 781; Conservative (INRM) INSERM INST NAT Perin J, WPI; 2000-160587/14. multiple sclerosis; 23-JUN-1999; 23-JUN-1998; W09967395-A1 29-DEC-1999. Alliel PM, 61 16 842 ABN97978; diseases. 1152 used RESULT 40 ABN97978 음. · 장 ద 유 g ð 1092 TAATAGAACTGAACACTGGTCACTGGGTTCCATGATCTCTTTCCATGACCCACGGCTTCT 1151

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17411, A
202370,
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Sequence 17382, A
Sequence 3, Appli
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Sequence 13002, A
Sequence 17417, A
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Sequence 21, App
Sequence 17411, 1
Sequence 202370,
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Sequence 15019, R
Sequence 13633, R
                                                                            February 21, 2005, 06:54:34; Search time 234.166 Seconds (without alignments) 9286.612 Million cell updates/sec
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(Ggn2_6/ptodata/1/ina/5A_COMB.seq:*
(Ggn2_6/ptodata/1/ina/5B_COMB.seq:*
(Ggn2_6/ptodata/1/ina/6A_COMB.seq:*
(Ggn2_6/ptodata/1/ina/6B_COMB.seq:*
(Ggn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
(Ggn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-949-016-44299
US-09-949-016-15019
US-09-949-016-13633
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US-09-949-016-17382

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US-09-949-016-13002

US-09-949-016-17417

US-09-949-016-17249

US-09-949-016-17249

US-09-949-016-17249

US-09-949-016-17420

US-09-949-016-17420

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Maximum Match 100%
Listing first 45 summaries
                                                     nucleic search, using sw model
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1329
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Perfect score:.
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TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYT
THERAPEUTIC PURPOSES
                                                                                                                                                                                                   Sequence 44297, A Sequence 44296, A Sequence 195792, Sequence 183390, Sequence 105, App Sequence 44310, A
                                                                                                                                                                 202257,
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MEDIUM TYPE: Floppy disk

COMPUTER: Floppy disk

COMPUTER: TBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/979, 847B

FLING DATE: 26-No. 6582703-1997

CLASSIFICATION: <Unknown>
US-09-949-016-11770
US-09-949-016-44300
US-09-949-016-195793
US-09-949-016-145543
US-09-949-016-146564
US-09-949-016-13399
US-09-949-016-133739
US-09-949-016-133739
US-09-949-016-126277
US-09-949-016-146565
US-09-949-016-146565
US-09-949-016-146565
US-09-949-016-146565
US-09-949-016-193390
US-09-949-016-193390
US-09-949-016-195794
US-09-949-016-195794
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NAME: BERRIDGS, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUTCATION INFORMATION:
TELEPHONE: 703-836-6400
TELEPHONE: 703-836-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
CITY: ALEXANDRIA
STATE: VA
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SRQUENCE DESCRIPTION: SEQ ID NO: 108:
US-08-979-847B-108
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FLORENCE
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Patent No. 6582703
GENERAL INFORMATION:
APPLICANT: PERRON, HERVE
BESEME, PREDERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BESEME, FREDERIC
BEDIN, FREDERIC
PARANHOS-BACCALA, G
KOMURIAN-PRADEL, FL
JOLIVET-REYNAUD, CO
MANDRAND, BERNARD
GARSON, JEREMY
TUKE, PHILIP
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27.9
27.9
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25.9
25.3
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1	1021	1081	1141	1201	1261 CCCACTGCCATTT	Oy 1321 CCAGTAACA 1329 Db 1321 CCAGTAACA 1329	RESULT 2 US-09-949-016-17382 ; Sequence 17382, Application US/09949016 · Datent No. 6812339	; GENERAL INFORMATION: ; APPLICANT: VENTER, J. Craig et al. ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND	; FILE REFERENCE: CL001307 ; CURRENT APPLICATION NUMBER: US/09/949,016 ; CURRENT FILING DATE: 2000-04-14 ; FRIOR APPLICATION NUMBER: 60/241,755	PRIOR FILING DATE: 2000-10-20 PRIOR APPLICATION NUMBER: 60/237,768 PRIOR FILING DATE: 2000-10-03 PRIOR PAPPLOATION NUMBER: 60/231.498	; PRIOR FILING DATE: 2000-09-08 ; NUMBER OF SEQ ID NOS: 207012 ; SOFTWARER FARESEQ for Windows Version 4.0 . SEC ID NO 17482	; LENGTH: 13592 ; LENGTH: 13597 ; TYPE: DNA ; ORGANISM: Human ; US-09-949-016-17382	Query Match 77.9%; Score 1035.2; DB 4; Length 13537 Best Local Similarity 90.1%; Pred. No. 0; Matches 1133; Conservative 0; Mismatches 111; Indels 13;	QY 1 TCAAAATCGAAGAGCTTTAGACTTGCTAACGGCAAAAGAGGGGGAACCTGTTT Db 10675 TCAAAATCGAAGAGCTTTAGACTTGCTAACGGCTGAAAGAGGGGGGAACCTGTTT	-	121 10795	181	241
5 A A	99.8%; Score 1326; DB 4; Length 1329; ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches 0; Indels 0; Gaps	aaaatcgaagagctttagacttggtaaccgccaaaagagggggaacctgtttattttt 	aggggaagaatgctgttagtatgttaatcaatctggaatcattactgagaaggttaaaga 	aattigagatggaatataatgtagagcagaggaccttcaaaacactgcacctggggcct 	CCTCAGCCAATGGATGCCCTGGACTCTCCCCTTCTTAGGACCTCTAGCAGCTATAATATT	TITACTCCTCTITGGACCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAATTTTACTCCTTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTTCGAGAATTTACTCCTCTTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTTCCTTC	TGAAGCTGTAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCACTCCATGACTAA 	AATCTACCGTGGACCCCCTGGACCGGCCTGCTAGACTATGCTCTGATGTTAATGACATTGA	AGTCACCCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTACACTCCCAATTCAGTAGG	AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTCCTGTTGAGA	GGGTGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCT	ANCTGGGAAGGTGACCGCATCCATTAAACATGGGGCTTGCAACTTAGCTCACACCGG	ACCAATCAGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCC 	AATCATCTATTGCCTGAGAGCACAGGGGAAGGACAAGGATTGGGATATAAACTCAGGCA 	TTCAAGCCAGCAACAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTT [CACTCTATTTCACTCTATTAAATCATGCAACTGCACTCTTCTGGTCCGTGTTTTTTATGG 	CTCAAGCTGAGCTTTTGTTCGCCATCCACTGCTGTTTGCCACCGTCACAGACCGCT	GCTGACTTCCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGGAGGT

CTGGGGCCT 180 |||||||||| |CTGGGGCCT 10854 TATAATATT 240 |||||||||| |TATAATATT 10914 TTCCAGAAT 300 |||||||||| |TTCCAGAAT 10974 AND USES THEREOF rrrarrrr 60 ||||||||||| |||||||||| AGTTAAAGA 120 |||||||||| AGTTAAAGA 10794 CTAAGTGCC 1080 |||||||||| CTAAGTGCC 1080 TTCCATGAC 1140 ||||||||| TTCCATGAC 1140 TCCTTGGTA 1200 |||||||||| |TCCTTGGTA 1200 GGGAAGTGG 1260 |||||||||| GGGAAGTGG 1260 AAGGATCCC 1320 ||||||||| AAGGATCCC 1320 ; Gaps

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APPLICANT: LaVallie, Edward R.
APPLICANT: COllins Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Evans, Cheryl
APPLICANT: Marchery, David
APPLICANT: Mr. Sha
APPLICANT: M. Sha
APPLICANT: Marches Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6006B.AJ172A
CURRENT FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN Ver. 2.0
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                      TTACTCCTCTTTGGACCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTTTCAGAAT
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                                                                                                                                                                                                                      Length 2946;
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                                                                                                                                                                           TYPE: DNA
CORGANISM: Homo sapiens
US-09-175-928-3
                                                                                                                                                                LENGTH: 2946
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                            TGAAGCTGTAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA
                                                                                                         AGTCACCCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGG
                                                                                                                                                     AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTCCTGTTGAGA
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US-09-175-928-3
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Sequence 3, Application US/09175928A Patent No. 6312921 GENERAL INFORMATION APPLICANT: Jacobs, Kenneth APPLICANT: McCOy, John M.

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Sequence 13002/C
; Sequence 13002/C
; Sequence 13002, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
   APPLICANT: VENTER, J. Craig et al.
   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
   TITLE OF INVENTION: WIMBER: US/09/949,016
   CURRENT PILING DATE: 2000-04-14
   PRIOR APPLICATION NUMBER: 60/231,768
   PRIOR APPLICATION NUMBER: 60/231,768
   PRIOR FILING DATE: 2000-10-03
   PRIOR FILING DATE: 2000-10-03
   PRIOR FILING DATE: 2000-09-08
   NUMBER OF SEQ ID NOS: 207012
   SOFTHARE: FREESE for Windows Version 4.0
   SEQ ID NO 13002
   LENTH: LESSON
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                                                                              541 GGGTGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCT
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Pred. No. 2.3e-237;
0; Mismatches 134;
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LOCATION: (1)...(168394)

OTHER INFORMATION: n = A,T,C or G

US-09-949-016-13002
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Best Local Similarity 85.0%;
Matches 878; Conservative
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| Sequence 5640, Application US/09949016
| Patent No. 681239
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al. |
| TITLE OF INVENTION: POLYMORPHSMS IN KNOWN GENES ASSOCIATED |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| FILE REPERENCE: CLOU3307 |
| CURRENT APPLICATION NUMBER: US/09/949,016 |
| CURRENT PILING DATE: 2000-04-14 |
| PRIOR APPLICATION NUMBER: 60/241,755 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-09-08 |
| NUMBER OF SEQ ID NOS: 207012 |
| SEQ ID NO 5640 |
| LENGTH: 2763 |
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               2775 AATCATCTATTGCCTGAGAGCACAGGAGGGACAATGATCGGGATATAAACCCAAGTC 2834
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                                                                   TTCAAGCCAGCAACAGCAACCCCTTTGGGTCCCCTCCCATTGTATGGGAGC
                                                                                                                                                                                                          CATGCTATTTCACTCTATTAAATCTTGCAACTGCA 2929
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Pred. No. 6.8e-239;
0; Mismatches 70;
                                                                                                                                                                   CACTCTATTTCACTCTATTAAATCATGCAACTGCA 875
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Best Local Similarity 90.6%;
Matches 792; Conservative
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; ORGANISM: Human
US-09-949-016-5640
                                                                                                                                                                                                                                                                                                   RESULT 4
US-09-949-016-5640
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                                                                                                                                                                                                                                                   Length 77772,
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49.3%; Score 654.8; DB 4;
Best Local Similarity 83.5%; Pred. No. 2.5e-212;
Matches 844; Conservative 0; Mismatches 140;
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER 00 SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4...
SEQ ID NO 17417
LENGTH: 77772
                                                                                                                                                                                                           G
                                                                                                                                                                              NAME/KEY: misc_feature

) LOCATION: (1)...(77772)

; OTHER INFORMATION: n = A,T,C or

US-09-949-016-17417
                                                                                                                                     TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            845
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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                          TATTGCCTGAGAGCACAGCGAAGGACAAGGATTGGGATATAAACTCAGGCATTCAAGC
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US-09-949-016-15858/C

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Requence 15959, Application US/09949016

Requence 15959, Application US/09949016

REQUENCE 15959, Application US/09949016

REPERANTION: VENTEN, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLOO1307 PORTOR APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 15858
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                                      CTAITITCACTCTATTAAATCATGCAACTGCACTCTTCTGGTCCGTGTTTTTTATGGCTCA
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Pred. No. 3.2e-208;
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Best Local Similarity
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; ORGANISM: Human
US-09-949-016-15858
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                                                                                                                                                                                                                                                                                                                                                                                                                      | Sequence 12249, Application US/09949016
| Sequence 12249, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER. V
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                                                                                                                                                                                                                                                                                                      27;
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                                                                                                                                                                                                                                                                           1203 IGTGAGGCCAAGAACCCCAGGTCAGAGAANGTGAGGCTTGCCACCATTGG
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49.3%; Score 654.8; DB 4;
Best Local Similarity 83.5%; Pred. No. 2.5e-212;
Matches 844; Conservative 0; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (1)...(77997)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12249
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LOCATION: (1)...(77997)
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US-09-949-016-12249/c
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CANT: ROGAN, PETER
PER INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES
PEFERENCE: 30307
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                                                                                                                                                              FEATURE:
NAME/KEY: rerpeat region
LOCATION: (1). (780)
OTHER INFORMATION: ltr17
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A
TITLE: Prototypic sequences for human repetitive DNA
JOURNAE: Journal of Molecular Evolution
VOLUME: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                            48.0%; Score 637.8; DB 4;
90.0%; Pred. No. 6.8e-208;
iive 0; Mismatches 60;
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            TITLE OF INVENTION: SINGLE COFF CONTROL OF THE REFERENCE: 30307
CURRENT APPLICATION NUMBER: US/09/573,080A
CURRENT FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 479
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                     PĀĞES: 286-291
DATE: 1992-10-
DATABASE ACCESTON NUMBER: Datak
DATABASE ENTRY DATE: --
DATABASE ENTRY DATE: 1996-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 90.0
Matches 711; Conservative
                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens
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Sequence 385, Application US/09573080A Patent No. 6828097 GENERAL INFORMATION: APPLICANT: JOAN, KNOLL

US-09-573-080A-385

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GENERAL INFORMATION:
APPLICANT: VERYER, J. Craig et al.
APPLICANT: VERYER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WINDER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NOS: 207012
SEQ ID NO 15086
LENGTH: 219964
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                                  142096 AGCTGAAGTTTCGCTCG-CGTCCACTGCTGTTTGCCGCTGTCACAGACCTGCCGCTG
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43.8%; Score 582; DB 4; I
Best Local Similarity 87.3%; Pred. No. 5.2e-187;
Matches 687; Conservative 0; Mismatches 83;
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; ORGANISM: Human
US-09-949-016-15086
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PELING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 245286
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                      CCCACGCTTCTAATAGAGCTATAACACTCACGCATGGCCCAAGATTCCATTCCTTGGA
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llarity 89.3%; Pred. No. 4.8e-205;
Conservative 0; Mismatches 82;
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; OTHER INFORMATION: n = A,T,C or
US-09-949-016-15497
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693; Conserv
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US-09-949-016-15497/c
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APPLICANT: VENTER, J Craig et al.
APPLICANT: VENTER, J Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER:
TILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: 06/241,755
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-37
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREEEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 17420
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                                      92314 GCCAACGCTACCCTCTTTGGGTCCCCTCCCTTTGTATGGGAGCTCTGT
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Patent No. 6812339
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LOCATION: (1)...(84571)
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OTHER INFORMATION: n =
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ORGANISM: Human
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RESULT 13
US-09-949-016-15393
US-09-949-016-15393
Sequence 15393, Application US/09949016
Sequence 15393, Application US/09949016
Sequence 15393, Application US/09949016
SEQUENCE TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
SEQUENCE TAPLICATION NUMBER: US/09/949,016
CURRENT PRILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
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|TCAGATAGTAAGGAGAGTCACTAAAATGCTAATTAGGCAAAAACAGGAGGTAAAGAAAT 7501
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                                                          ACTGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAA-GAATCCCNAAGCCTANCTG
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86.5%; Pred. No. 1.1e-181; ive 0; Mismatches 82;
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99199 GGCCGCCCCATCTTGGGAGTGGCCAC 99225
                                                                                 ; Sequence 102, Application US/08979847B ; Patent No. 6582703 ; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 635 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 102:
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92.4%;
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Best Local Similarity 92.4
Matches 572; Conservative
                                                                      US-08-979-847B-102
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                                                                                                                                                                                                     21;
                                                                                                                                                                            Length 194790;
                                                                                                                                                                        Query Match
42.3%; Score 562; DB 4; Length 19
Best Local Similarity 82.8%; Pred. No. 3.5e-180;
Matches 718; Conservative 0; Mismatches 128; Indels
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    PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FABLSEQ for Windows Version 4.0
SEQ ID NO 15393
                                                                                                                       TYPE: DNA
ORGANISM: Human
                                                                                                                                                US-09-949-016-15393
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TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
THERAPEUTIC PURPOSES
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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Pred. No. 4.3e-176;
0; Mismatches 47;
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APPLICATION NUMBER: US/08/979,847B
FILING DATE: 26-No. 6582703-1997
CLASSIFICATION: «Unknown»
ATTORNEY AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REGISTRATION INFORMATION:
TELEPHONE: 703-836-6400
                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
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MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 102:
US-08-979-847B-102
APPLICANT: PERRON, HERVE
BESEME, FREDERIC
BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
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JERURALI INFORMATION:

JAPPICANT: VENTEL N.

JAPPICANT: VENTELN.

JITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

JITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

JITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRASESQ for Windows Version 4.0

SEQ ID NO 13413

LENGTH: 116652
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; Patent No. 6812339
; GENERAL INFORMATION:
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OTHER INFORMATION: n = A,T,C
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ORGANISM: Human
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Sequence 17002 Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFRENCE: CLOA01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FESTSEQ for Windows Version 4.0
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       GAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGAAGCAGTTAGAGCGGT 240
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                                                                                                            AGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCTANCTGGGAAGGTGACC
                                                                                                                                301 AGGACTAGCTAGCTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGAAGATGACT
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82.4%; Pred. No. 4.6e-159;
iive 0; Mismatches 106;
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Best Local Similarity 82.4
Matches 631; Conservative
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-09-949-016-17002
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LENGTH: 140224
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US-09-949-016-11757/c
US-09-949-016-11757/c
Sequence 101757, Application US/09949016
Patent No. 681239
GENERAL INFORMATION:
PAPLICANT: WENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WINDER: US/09/949,016
CURRENT APPLICATION NUMBER: 05/04-14
PRIOR APPLICATION NUMBER: 60/241,755
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                                           547 ACTGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCTANCT-G
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Score 478.6; DB 4;
Pred. No. 1.1e-151;
0; Mismatches 102;
 36.0%;
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Query Match
Best Local S
Matches 671
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Pred. No. 3.1e-148;
0; Mismatches 102;
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 11757
LENGTH: 131631
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Best Local Similarity 83.3%;
Matches 645; Conservative
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LOCATION: (1)...(13163:
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FEATURE:
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Sequence 17057, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRAESEQ for Windows Version 4.0

SEQ ID NO 17057
                                                                                                           55341 GAAGCAGCCTGCCACCATCTTGGAAGCAGCCTGCCACCATCTTGGGAGCTCTGGGAGCAA 65282
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Pred. No. 2e-140;
0; Mismatches 118; Indels 22;
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Best Local Similarity 81.3%;
Matches 607; Conservative
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US-09-949-016-17057
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                        Sequence 1708, Application US/09949016

Sequence 1708, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERENCE: CLOOL337

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-3

PRIOR FILING DATE: 2000-10-3

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 17068

LENGTHREE FASTES OF WINDOWS VEISION 4.0

SEQ ID NO 17068

LENGTHREE FASTES
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Pred. No. 7.2e-148;
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Best Local Similarity 81.2%;
Matches 639; Conservative
                      -09-949-016-17068/c
                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17068
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Gaps

92413

92473

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Sequence 11973, Application US/09949016

Sequence 11973, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VEXTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-010-03

PRIOR PELING DATE: 2000-010-03

PRIOR PELING DATE: 2000-010-03

SPRIOR FILING DATE: 2000-010-03

SPRIOR FILING DATE: 2000-010-03

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LOCATION: (1)...(251682)
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Human
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Best Local Simi
Matches 599;
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOJ307
CURRENT APPLICATION NUMBER: 06/241,755
PRIOR FILING DATE: 2000-00-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTHARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 17296
LENGTH: 251672
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                                                                                          92707 GGGAGGCGCCCATIGCCGCTCCCGATCAGGCTAGAGGCTTGCTAGTTCCTGCGTGGCT
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| LOCATION: (1)...(251672)
| OTHER INFORMATION: n = A,T,C or G
| US-09-949-016-17296
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Matches 599; Conserv
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US-09-949-016-17296
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## Sequence 1741, Application US/09949016
## Sequence 1741, Application US/09949016
## Sequence 1741, Application US/09949016
## Setent No. 681239
## Setent No. 681239
## Setent No. 681239
## Setent No. 681239
## Setent No. 681239
## SETENT ON TOWERTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
## TITLE OF INVERTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
## CURRENT APPLICATION NUMBER: US/09/949,016
## PRIOR APPLICATION NUMBER: 60/241,755
## PRIOR FILING DATE: 2000-10-03
## PRIOR FILING DATE: 2000-10-03
## PRIOR APPLICATION NUMBER: 60/237,768
## PRIOR FILING DATE: 2000-10-03
## PRIOR APPLICATION NUMBER: 60/231,498
## PRIOR APPLICATION NUMBER: 60/231,498
## PRIOR FILING DATE: 2000-09-08
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                                                                                                                   of repetitive elements (repbase)
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Prototypic sequences for human repetitive DNA .: Journal of Molecular Evolution
                                                                                                                                                                                                               Score 440.4; DB 4;
Pred. No. 2.2e-139;
0; Mismatches 46;
                    JOURNAL: Journal of Molecular Evolution VOLUME: 35 ISSUE: 18SUE: 18SUE: 198-291 DATE: 1992-10-DATABASE ACCESSION NUMBER: Database of DATABASE ENTRY DATE: DATABASE ENTRY DATE: 1996-01-26
                                                                                                                                                                                                                 Query Match
Best Local Similarity 89.4%;
Matches 490; Conservative
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US-09-949-016-17411/c
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US-09-573-080A-21
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                                                                                                                        12753 CAGGTAGTAAAGAGGGCTCACTAAAATACAAATTAGGCTAAGAGGAGGAGGTAAAGAAAT
                                                                                                                                                                AG-CCAATCATCTATTGCCTGAGAGCACAGCGGAAGGACAAGGATTGGGATATAAA-CT
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LOCATION: (1)..(8523)
OTHER INFORMATION: PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: JOAN, KNOLL
APPLICANT: OCAN, PETER
TITLE OF INVENTION: SINGLE COPY GENOMIC HYB:
FILE REFERENCE: 30307
CURRENT APPLICATION NUMBER: US/09/573,080A
CURRENT APPLICATION NUMBER: US/09/573,080A
NUMBER OF SEQ ID NOS: 479
SOFTWARE: Patentin version 3.0
SEQ ID NO 8523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 22
US-09-573-080A-21
Sequence 21, Application US/09573080A
; Patent No. 6828097
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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SQUENCE 44299, Application US/09949016

Badent No. 6812339
GENERAL INFORMATION:
PAPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF CURRENT APPLICATION NUMBER: 08/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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                                                                                                                                   Length 601;
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                                                                                                                                Query Match 32.7%; Score 434.8; DB 4; Best Local Similarity 86.0%; Pred. No. 2.9e-138; Matches 520; Conservative 1; Mismatches 69;
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 202370
LENGTH: 601
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US-09-949-016-44299/c
                                                                                                         US-09-949-016-202370
                                                                              TYPE: DNA
ORGANISM: Human
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF PILE REPERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PELING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03
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                                                                                                                                                         Gaps
                                                                                                                                                         12;
                                                                                                                        Length 99580;
                                                                                                                                                         Indels
                                                                                                                           DB 4;
                                                                                                                           Score 435.8; DB 4.
Pred. No. 4.7e-137
0; Mismatches 74
      NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 17411
LENGTH: 99580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-949-016-202370/c
; Sequence 202370, Application US/09949016
; Patent No. 6812339
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                                                                                                                               32.8%;
86.1%;
                                                                                                                                                            Matches 531; Conservative
                                                                                                                                             Similarity
                                                                                 ; ORGANISM: Human
US-09-949-016-17411
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                                                                      TYPE: DNA ORGANISM:
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Best Local
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, ORGANISM: Human
US-09-949-016-15019
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                                                                                 TYPE: DNA ORGANISM:
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Batent No. 6812339

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR PLILING DATE: 2000-10-20
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                                                                                                                                          Gaps
                                                                                                                                          17;
                                                                                                                    601;
                                                                                                                    Length
                                                                                                                                          Indels
                                                                                                                  Score 427.8; DB 4;
Pred. No. 7.3e-136;
1; Mismatches 80;
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 44299
LENGTH: 601
                                                                                                                   Query Match
Best Local Similarity 83.9%;
Matches 511; Conservative
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                                                                                 , ORGANISM: Human
US-09-949-016-44299
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                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                    31.0%; Score 411.4; DB 4; 79.6%; Pred. No. 7.6e-129; iive 0; Mismatches 124;
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBERS: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15019
LENGTH: 57507
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; Sequence 13633, Application US/09949016
; Patent No. 6812339
; GRNERAL INFORMATION:
                                                                                                                                                                                                                                                                                Matches 592; Conservative
                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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General 11770, Application US/09949016

patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOOD1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PRESEEQ for Windows Version 4.0
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                                                     1231 ANGTGAGGCTTGCCACCATTTGGGAAGTGGCCCACTGCCATTTTGG 1276
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                                                                            Query Match 30.1%; Score 399.8; DB 4; Best Local Similarity 78.1%; Pred. No. 6.6e-125; Matches 598; Conservative 0; Mismatches 120;
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LOCATION: (1).7.(49487)
OTHER INFORMATION: n = A,T,C or G
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-09-949-016-11770/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human
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US-09-949-016-11770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 11770
LENGTH: 49487
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     APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOO1307;
CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR PLING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOMMARE: FRAKESQ for Windows Version 4.0

SEQ ID NO 13633
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 399.8; DB 4; Length
Pred. No. 5.7e-125;
0; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (1)...(39686)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 78.1%;
Matches 598; Conservative
                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Human
FEATURE:
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US-09-949-016-195793/C

US-09-949-016-195793, Application US/09949016

Paquence 195793, Application US/09949016

Patent No. 6812139

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PAPLICATION NUMBER: 60/241,755

PRIOR PAPLICATION NUMBER: 60/237,768

PRIOR PAPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FESTSEQ for Windows Version 4.0

LENGTH: 601
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                   TATTGCCTGAGAGCACAGCGGGAAGGACAAGGATTGGGATATAAACTCAGGCATTCAAGC 787
                                                                                           136 AGAGAGTTCACTAAAATGCTAACTAGGCAAAAACAGGAGGTAAAGAAATAGCCAATCATC 77
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Pred. No. 2.3e-116;
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82.3%; Pred. No. a...
1; Mismatches
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Matches 487; Conservative
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IS-69-949-016-44300, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PLILOR DATE: 2000-10-20

PRIOR PELICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRALSEQ for Windows Version 4.0

SEQ ID NO 44300
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                                                                                                                                      CTTGCCATTGTTCCTGCATGGCTAAGTGCCTGGGTTTGTCCTAATAGAACTGAACACTGG
                                                                                                                        TCACTGGGTTCCATGGTTCTCTTCCATGACCCACGGCTTCTAATAGAGCTATAACACTCA
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                                                                                                                                                                                                                                                                                   Length 601;
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Pred. No. 5.4e-122;
1; Mismatches 64;
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Best Local Similarity 85.9%;
Matches 477; Conservative 1
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US-09-949-016-44300
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1244 CACCATTTGGGAAGTGGCCCACTGCCATTTTGGTAGC
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Best Local Similarity 83.7%;
Matches 405; Conservative 1
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastESQ for Windows Version 4.0
SEQ ID NO 44298
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                                                                                    CGGCTTCTAATAGAGCTATAACACTCACCGCATGGCCCAAGATTCCATTCCTTGGTATCT 1203
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                                                      174 Gricercciaarcaagcicaacacraarcgcreecriceaceacricicrercrergarca 115
CGTIGCIGCICCIGATIGGGCIAAAGGCICACCATIGIICCIGCACAGCIAAGIGCCIGG 175
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                                                                                                                                                               Length 601;
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Pred. No. 7e-116;
1; Mismatches 76; Indels
                                                                                                                                                                                                                                           Sequence 44298, Application US/09949016
Patent No. 6812339
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Best Local Similarity 83.6
Matches 432; Conservative
                                                                                                                                                                                                                   RESULT 31
US-09-949-016-44298/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-44298
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Sequence 146564, Application US/09949016

Sequence 146564, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VBYTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS: METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WIMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTHARE: PSELSE for Windows Version 4.0

SEQ ID NO 146564

LENTH: 601
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1036 CGATCAGGCTAAAGGCTTGCCATTGTTCCTGCATGGCTAAGTGCCTGGGTTTGTCCTAAT
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Pred. No. 1.4e-107;
1; Mismatches 68;
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; Sequence 133739, Application US/09949016
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US-09-949-016-133739/c
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Patent No. 6812339
GRNERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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                         Sequence 21394, Application US/09513999C

Fatent No. 6783961

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFREENCE: 59 US2.RED

FILE REPERENCE: 59 US2.RED

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SEQ ID NO 21394

LENGTH: 443
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US-09-513-999C-21394
                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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LOCATION: 102
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US-09-949-016-13590/c
RESULT 33
US-09-513-999C-21394
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25.9%; Score 343.6; DB 4; Length 149971;
Best Local Similarity 79.7%; Pred. No. 2.9e-105;
Matches 488; Conservative 0; Mismatches 96; Indels 28;
           CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                           | NAME/KEY: misc_feature
| LCCATION: (1)...(149971)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13590
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CL001307
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; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 120277; LENGTH: 601
; TYPE: DNA; ORGANISM: Human
US-09-949-016-120277
                                                                                                                                         Query Match 25.3%;
Best Local Similarity 86.2%;
Matches 394; Conservative
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| Sequence 120277, Application US/09949016
| Patent No. 681239
| GENERAL INFORMATION
| APPLICANT: VENTER, J. Craig et al. APPLICANT: VENTER, J. Craig et al. APPLICANT: VENTER, J. Craig et al. APPLICANT: VENTER V. TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; FILE REPRENCE: CL001307
| TITLE OF INVENTION: WINBER: US/09/949,016
| CURRENT APPLICATION NUMBER: 60/241,755
| PRIOR PLILING DATE: 2000-10-20
| PRIOR PLILING DATE: 2000-10-03
| PRIOR PLILING DATE: 2000-10-03
| PRIOR PLILING DATE: 2000-09-08
| PRIOR APPLICATION NUMBER: 60/231,498
| PRIOR PLILING DATE: 2000-09-08
| WINDHER OF SEQ ID NOS: 207012
                      GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FaetSEQ for Windows Version 4.0
LENGTH: 601
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Best Local Similarity 89.9
Matches 372; Conservative
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; ORGANISM: Human
US-09-949-016-133739
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Sequence 20257, Application US/09949016

Sequence 20257, Application US/09949016

Betent No. 681239

GENERAL INFORMATION:
APPLICANTY VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFREENCE: L2000.1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOCTHARE: FastSEQ for Windows Version 4.0

LENGTH: 601
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Score 336; DB 4; Pred. No. 2.4e-104; 1; Mismatches 57;
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Sequence 44297, Application US/09949016
; Sequence 4223, Application US/09949016
; Patent NO. 681239
; GENERAL INFORMATION:
    TITLE OF INVENTEN, J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; CURRENT PAPLICATION NUMBER: 00/241,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR PILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; LENGTH- 601
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                                                                               1096 AGAACTGAACACTGGTTCACTGGTTCCATGTTCTTCCATGACCCACGGCTTCTAATA
                                                                CGATCAGGCTAAAGGCTTGCCATTGTTCCTGCATGGCTAAGTGCCTGGGTTTGTCCTAAT
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23.9%; Score 317.6; DB 4; Length
Best Local Similarity 86.0%; Pred. No. 5e-98;
Matches 350; Conservative 1; Mismatches 56; Indels
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TCACTCTATTAAATCATGC 868
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                                                                                                                                                                                                                                                                                                       293 AGTCCCTGRGTTCCAAGTTCTCTTCCATGACCCACGCCTTCTAATAGAGCTATAACACT
                GGTACCCCCCGGTTGAATGGGAGCTCTGTTTTCACTCTATTAAATCTTGCAACTGCA---
                                                                                                               CCACTGCTGTTTGCCACCGTCACAGACCCGGTGCTGACTTCCATCCCTTTGGATCCAGCA
                                                       869 AACTGCACTCTTCTGGTCCGTGTTTTTTATGGCTCAAGCTGAGCTTTTGTTCGCCATCCA
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Pred. No. 4.3e-98;
1; Mismatches 53
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Best Local Similarity 85.2%;
Matches 369; Conservative
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US-09-949-016-146565
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US-09-949-016-146565
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RESULT 40

US-09-949-016-44296/c

J Gequence 44296, Application US/09949016

Patent No. 681233

GENERAL INPORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOL1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PLLING DATE: 2000-10-03

PRIOR PLLING DATE: 2000-10-03

PRIOR PLLING DATE: 2000-10-03

PRIOR PLLING DATE: 2000-10-03

PRIOR PLLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PESELSEQ for Windows Version 4.0

LENGTH: 601
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292 CATGGCCCAAGATTCCATTCTTTGGAACCTTTGAGGCCAAGAACCCCAGGTCAGAGAACA 233
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                                     1234 TGAGGCTTGCCACCATTGGGAAGTGGCCCACTGCCATTTTGGTAGC 1280
                                                               232 AGAGGCTTGCCGCTATCTTGGAAGGGGCCTGCCACCATCTTGGGAGC 186
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CRGANISM: Human
US-09-949-016-44296
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February 21, 2005, 11:52:50; Search time 734.518 Seconds (without alignments) 10694.149 Million cell updates/sec
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15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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10: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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1329
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 108, App	Sequence 108, App	Sequence 81, Appl	Sequence 910, App	Sequence 17, Appl	Sequence 18, Appl	Sequence 9936, Ap	Sequence 4, Appli	Sequence 134, App	Sequence 3, Appli	Sequence 1, Appli
ΩΙ	8 US-08-979-847-108	US-10-114-104-108	US-09-873-367C-81	US-10-087-192-910	US-10-220-120-17	US-10-637-565-18	US-10-198-846-9936	US-10-416-642-4	US-10-114-893-134	US-10-016-249-3	US-09-902-535-1
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% Query Match Length DB	1329	1329	56093	21646	1393	2030	7974	2074	2946	2946	2930
% Query Match	99.8	99.8	77.9	60.1	58.6	58.3	58.3	57.7	55.1	55.1	55.0
Score	1326	1326	1035.2	798.2	778.8	775.4	774.2	766.8	731.8	731.8	730.8
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	-632-7	-10-632-793	632-7	133-0	-864-761	087-1	854-8	741-6	672-7	003-8	003-8	017-1	240-4	-979-847-102	114-1	220-1	719-9	741-6	264-2	31-23	751-9	719-9	1-741-600-17995	US-10-719-993	0-741-600	-10-276-774-67	632-7	7-766.	.087-1	027-6	027-6	-10-637-565-1	0-637-565-1	-864-761-7
	US-10-	US-10-	JS-10-	US-10-133-036	8-60-8	US-10-087-192-7	US-09-854-867	US-10-741-600-1	US-10-	US-10-	US-10-003-806-9	US-10-	US-10-240-425-11	US-08-5	US-10-	US-10-220-120-15	US-10-719-993-6'	US-10-741-600-17	US-10-264-237-2	US-09-731-231A-3	US-10-	US-10-719-993-706	US-10-	US-10	US-10	US-10-	US-10-	US-09-997-722-148	US-10.	US-10-	US-10-	US-10-637-565-1	US-10-	3-60-SD
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	54.4	54.3	53.6	53.5	53.0									41.0	41.0	40.3			38.5	37.8	37.8	36.0												34.1
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TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRACMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
THERAPEUTIC PURPOSES
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CTGGTCCGTGTTTTTATG
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                                                                                                         GCTGACTTCCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGCGAGGT
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                                            CACTCTATTTCACTCTATTAAATCATGCAACTGCACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, ENT APPLICATION DATA:
APPLICATION NUMBER: US/10/114,104 PILING DATE: 03-APr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BESEME, FREDERIC
BEDIN, FREDERIC
PARANHOS-BACCELA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
MANDRAND, BERNARD
GARSON, JERBYY
TUKE, PHILIP
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CORRESPONDENCE ADDRESS:
ADDRESSE: OLIFE & BERRIDGE, PL
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 108, Application US/10114104; Publication No. US20030198647A1; GENERAL INFORMATION:
APPLICANT: PEREOK. HERVE
BESEME, FREDERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAGTAACA 1329
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99.8%; Score 1326; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1329; Conservative 0; Mismatches
         ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
TELEPAX: 703-836-6400
TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 1329 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: STRANDEDNESS: Single
                                                                                                                                                                                    MOLECULE TYPE: CDNA
                                                                                                                                                                        linear
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US-08-979-847-108
                                                                                                                                                                        TOPOLOGY:
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CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: 08/979,847

**PILING DATE: 26-NOV-1997

**FILING DATE: 26-NOV-1997

**ATORNEY/AGENT INFORMATION:

**NAME: BERRINGE, WILLIAM P.

**REGISTRATION NUMBER: 30,024

**REGISTRATION NUMBER: 30,024

**RETERENCE/DOCKET NUMBER: WPB 39046A

**TELECOMUNICATION INFORMATION:

**TELEPHONE: 703-836-640

**TELEPHONE: 703-836-640

**TELEPHONE: 703-836-640

**TELEPHONE: 703-836-640

**TELEPHONE: TOWN: 108:

**SEQUENCE CHARACTERISTICS:

**LENGTH: 1329 base pairs

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; Sequence 910, Application US/10087192
; Bublication No. US2002018286A1
; GENERAL INFORMATION:
    APPLICANT: Morris, David W.
; APPLICANT: Morris, David W.
; TITLE OF INVENTION: ONDEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: OANCER.
; TITLE OF INVENTION: OANCER.
; FILE REFERENCE: 52945200122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSEQ for Windows Version 4.0
; TENGTH. 216.64
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// ICCATION: (1)...(21646)

// OTHER INFORMATION: n = A,T,C or

US-10-087-192-910
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ORGANISM: Homo sapiens
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US-10-087-192-910
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                                                                                                   Gaps
                                                                       DB 10; Length 56093;
                                                                                                   13;
                                                                    Score 1035.2; DB 10; Lengt
Pred. No. 1.6e-310;
0; Mismatches 111; Indels
                                                                    Query Match
Best Local Similarity 90.1%;
Matches 1133; Conservative C
      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-367C-81
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60/184,770; 60/184,774
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OTHER INFORMATION: Incyte ID No. US20040048253A1 LI:351965.1:2000FEB01
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Pred. No. 1.9e-231;
0; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: 120, 765
; OTHER INFORMATION: a, t, c, g, or other
US-10-220-120-17
                                                                                                            Χ.
                                                                                                          STOCKDREHER, Theresa
                LLMAN, Jennifer L
NES, Anissa L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 58.6%;
Best Local Similarity 87.2%;
Matches 904; Conservative
                                              LIU, Tommy F.
ROSEBERRY, Ann M.
ROSEN, Bruce H.
RUSSO, Frank D.
                                                                                                                            DAFFO, Abel
WRIGHT, Rachel J.
YAP, Pierre E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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CTGCTGACTTCCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGCGAG 1018
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US-10-220-120-17
Sequence 17, Application US/10220120
Publication No. US20040048253A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: SPIRO, Peter A.
APPLICANT: BANVILLE, Steven C.
APPLICANT: BANVILLE, Steven C.
APPLICANT: GHALIP, Michael S.
APPLICANT: GHALIP, Michael S.
APPLICANT: GHALIP, Michael S.
APPLICANT: GHALIP, Michael S.
APPLICANT: GHALIP, Michael S.
APPLICANT: D'SA, Steven A.
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APPLICANT: D'SA, Steven A.
APPLICANT: D'SA, Steven B.
APPLICANT: DAM, Tam C.
APPLICANT: DANIELS, Susan E.
APPLICANT: PLONES, Vincent
APPLICANT: FONG, Willy T.
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                                                                                                                                                                                     Length 2030;
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                                                                                                                                                                                  Score 775.4; DB 17;
Pred. No. 2.7e-230;
0; Mismatches 63;
PRIOR APPLICATION NUMBER: EP 99420041.8
PRIOR FILING DATE: 1999-02-15
NUMBER OF SEQ ID NOS: 20
SCFWARE: Patentin version 3.0
SEQ ID NO 18
LENGTH: 2030
                                                                                                                                                                                   58.3%;
92.8%;
                                                                                 TYPE: DNA

ORGANISM: MSRV-1 retrovirus

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(1626)

US-10-637-565-18
                                                                                                                                                                                                  Best Local Similarity 92.8
Matches 812; Conservative
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APPLICANT: PERRON Herve
APPLICANT: PERRON Herve
APPLICANT: PERRON Herve
APPLICANT: WOUNTIAN PRADEL, Florence
TITLE OF INVENTION: THE LITR REGION OF WSRV-1 AND THE PROTEINS IT ENCODES, AND PROBES
FILE REPERENCE: 110257
FILE REPERENCE: 110257
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: US/09/890,340
PRIOR APPLICATION NUMBER: PCT/IB00/00159
PRIOR APPLICATION NUMBER: PCT/IB00/00159
PRIOR FILING DATE: 2000-02-15
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OTHER INFORMATION: Incyte ID No. US20040043452A1 7477736CB1
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Bublication No. US20040043452A1

GENERAL INFORMATION:

APPLICANT: INCYEE GENOMICS, INC.

APPLICANT: RAMKUMAR, JAYALAMI

TILLS OF INVENTION: BMBRYGGENESIS ASSOCIATED PROTEINS
FILE REFERENCE: PF-0842 PCT

CURRENT FILING DATE: 2003-05-13

PRIOR APPLICATION NUMBER: 06/249,407

PRIOR FILING DATE: 2000-11-15

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PERL PROGram

SEQ ID NO 4
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Pred. No. 1.3e-227;
0; Mismatches 60;
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; OTHER INFORMATION: a,
_US-10-416-642-4
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Best Local Similarity
Matches 812; Conserv
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US-10-416-642-4
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                                                                                                                                                                          APPLICANT: Lillie, James
APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wangy Youzhao
APPLICANT: Wangy Youzhao
APPLICANT: Wangy Youzhao
APPLICANT: Wangy Youzhao
APPLICANT: Wangy Youzhao
TITLE OF INVENTION: POR IDENTIFICATION ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT PILING DATE: 2002-07-18
FRIOR APPLICATION NUMBER: 60/306,220
PRIOR PELING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9936
LENGTH: 7974
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Pred. No. 1.3e-229;
0; Mismatches 126;
                 841 CACTCTATTTCACTCTATTAAATCATGCAACTGCA
                                                                                                                        Sequence 9936, Application US/10198846
Publication No. US20030099974A1
GENERAL INFORMATION:
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Best Local Similarity 85.8%;
Matches 937; Conservative
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US-10-198-846-9936
                                                                                         RESULT 7
US-10-198-846-9936
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Publication No. US20020193567A1
GENERAL INFORMATION:
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Evans, Cheryl
APPLICANT: Evans, Cheryl
APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Reacy, Maurice
APPLICANT: Reacy, Maurice
APPLICANT: Reacy, Maurice
APPLICANT: Spaulding, Vikki
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US-10-114-893-134
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APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Kelleher, Kerry S.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETE PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: GI 6000-10A
CURRENT APPLICATION NUMBER: US/10/114,893
CURRENT APPLICATION NUMBER: US/10/114,893
CURRENT APPLICATION NUMBER: 09/413,232
EARLIER FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 321
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 134
LENGTH: 2946
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Pred. No. 1.3e-216;
0; Mismatches 69;
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Best Local Similarity 90.7%;
Matches 794; Conservative 0
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CORGANISM: Homo sapiens
US-10-114-893-134
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APPLICANT: Keith, Jr., James C.
APPLICANT: Mi, Sha.
APPLICANT: Mi, Sha.
TITLE OF INVENTION: Methods and compositions for diagnosing
TITLE OF INVENTION: and treating preeclampsia and gestational trophoblast
TITLE OF INVENTION: disorders
FILE REFERENCE: GIN-600648
CURRENT APPLICATION NUMBER: US/09/902,535
CURRENT APPLICATION NUMBER: 60/216,657
PRIOR APPLICATION NUMBER: 60/216,657
PRIOR FILING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1.
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Pred. No. 2.7e-216;
0; Mismatches 69;
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Best Local Similarity 90.7%;
Matches 793; Conservative (
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LOCATION: (930)...(2546)
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Sequence 3, Application US/10016249;
Publication No. US20030100053A1
GENERAL INPORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Treacy, Maurice
APPLICANT: Fracy, Maurice
APPLICANT: Werberg, David
APPLICANT: Merberg, David
APPLICANT: Merberg, David
APPLICANT: Merberg, Maurice
APPLICANT: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
TITLE OF INVANTION: SECRETED PROTEINS.
TITLE OF INVANDER: 2001-10-30
TITLE REFERENCE: 6006B.AJ172A
CURRENT APPLICATION NUMBER: US/10/016,249
CURRENT FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LEBUTAL DATE:
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Pred. No. 1.3e-216;
0; Mismatches 69;
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TTTACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAAT
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88.5%; Pred. No. 1.6e-213;
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Best Local Similarity 88.5%;
Matches 774; Conservative
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NAME/KEY: misc feature
LOCATION: (3787)..(3787)
OTHER INFORMATION: n = a or
FEATURE:
NAME/KEY: misc feature
LOCATION: (4115)..(4115)
OTHER INFORMATION: n = a or
                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (2213) ..(2213)
OTHER INFORMATION: n = a
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2398) ..(2398)
OTHER INFORMATION: n = a
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COCATION: (4261). (4261)

COTHER INFORMATION: n = a

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       FEATURE:
NAME/KEY: misc feature
LOCATION: (307)..(307)
OTHER INFORMATION: n = a
FEATURE:
NAME/KEY: misc feature
LOCATION: (355)..(355)
OTHER INFORMATION: n = a
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NAME/KEY: misc feature
LOCATION: (1331)..(1331)
OTHER INFORMATION: n = a
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LOCATION: (1309)...(1309)
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                                                                 CCTCAGCCAATGGATGCCCTGGACTCTCCCCTTTAGGACCTCTAGCAGCTATATTT
             CATECTATTCACTCTATTAAATCTTGCAGCTGC 1115
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                                            AAGCAGTTAGAGCGGTSGTCGGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGA
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                     AGTCACCCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGG
                                                                                            AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGGTTTTCCTGTTGAGA
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90.0%; Pred. No. 1.6e-213;
live 0; Mismatches 75;
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US-10-632-793-25
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Pred. No. 1.2e-210;
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SOFTWARE: PatentIn version 3.1
                                                           Query Match
Best Local Similarity 89.4%;
Matches 782; Conservative
                        TYPE: DNA
ORGANISM: Homo sapiens
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                                                            APPLICANT: Contad. Bernard
APPLICANT: Contad. Bernard
TITLE OF INVENTION: Multiple Sclerosis-Related Superantigen
TITLE OF INVENTION: Multiple Sclerosis-Related Superantigen
FILE REFERENCE: 23135-507
CURRENT APPLICATION NUMBER: US/10/133,036
CURRENT FILING DATE: 2002-04-26
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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89.3%; Pred. No. 3.9e-210;
tive 0; Mismatches 82;
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Sequence 1, Application US/10133036; Publication No. US20040054133A1; GENERAL INFORMATION:
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Best Local Similarity 89.3'
Matches 781, Conservative
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OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 5.9 OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.2 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.9 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.2 US-09-864-761-4444
                                                                                                                                                                                   Score 704.8; DB 9;
Pred. No. 2.7e-208;
0; Mismatches 79;
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llarity 89.7%;
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Matches 770; Conserv
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                                                                                                                                                                                                                                                                                                                                         PREMERAL, INFORMATION APPLICANT: Bent, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

TITLE OF INVENTION: GREE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Accordica-X-1

CURRENT APPLICANTON WUNDER: US 60/180, 312

REIOR PLILNG DAYE: 2000-10-23

REIOR PLILACATION WUNDER: US 60/180, 312

REIOR APPLICATION WUNDER: US 60/180, 312

REIOR APPLICATION WUNDER: US 60/180, 312

REIOR PLILACATION WUNDER: US 60/180, 316

REIOR PLILACATION WUNDER: US 60/180, 316

REIOR PLILACATION WUNDER: US 60/180, 316

REIOR PLILACATION WUNDER: US 60/180, 316

REIOR PLILACATION WUNDER: US 60/180, 316

REIOR PLILACATION WUNDER: US 60/180, 316

REIOR PLILACATION WUNDER: US 60/180, 316

REIOR PLILACATION WUNDER: US 60/180, 316

REIOR PLILACATION WUNDER: US 60/180, 316

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REIOR PLILACATION WUNDER: US 60/180, 316

REIOR PLILACATION WUNDER: US 60/180, 316

REIOR PLILACATION WUNDER: US 60/180, 408

REIOR APPLICATION WUNDER: US 60/180, 408

REIOR APPLICATION WUNDER: US 60/180, 408

REIOR APPLICATION WUNDER: US 60/180, 408

REIOR APPLICATION WUNDER: US 60/180, 408

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REIOR APPLICATION WUNDER: US 60/180, 408

REIOR REIOR APPLICATION WUNDER: US 90/174, 203

REIOR REIOR APPLICATION WUNDER: US 90/180, 408

REIOR REIOR APPLICATION WUNDER: US 90/174, 203

RENORMAN PRINCE WILL SOULD SO
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.4
                                                                                                                                                                               2730 CATGCTATTTCACTCTATTAAATCTTGCAACTGCA 2764
                                                                                                                                                      CACTCTATTTCACTCTATTAAATCATGCAACTGCA 875
                                                                                                                                                                                                                                                                                       Sequence 4444, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Sequence 385, Application US/09854867

Publication No. US20030224356A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GOAN, KNOLL H

APPLICANT: ROGAN, ENGLE H

TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING;
TITLE REFERENCE: 30307

CURRENT APPLICATE: 2003-05-08

NUMBER OF SEQ ID NOS: 613

SOFTWARE: PATENTIN VETSION 3.1

SEQ ID NO 385

LENGTH: 780
               100298 TITCCTAGGCCGACTAAGAATCCCAAAGCCTAGCTGGGAAGGTGACCACACCCTTTA 100239
                                                                          100238 AACACTGGGCTTGCAACTTAGCTCACCCGACCAATCAGGTAGTAAAGAGAGCTCACTA 100179
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                                                 AACATGGGGCTTGCAACTTAGCTCACCGACCAATC-----AGAGAGCTCACTA
                                                                                                         AAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCCAATCATTGTTTGCCTGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 637.8; DB 10; Length 780;
Pred. No. 1.3e-187;
0; Mismatches 60; Indels 19;
TTTCCTAGGCTGACTAAGAATCCCNAAGCCTANCT
                                                                                                                                                                                                                                                                                                      Query Match 48.0%;
Best Local Similarity 90.0%;
Matches 711; Conservative 0
                                                                                                                                                                                                                                                                                      AATCATGCAACTGCA 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: rerpeat_region; CCATION: (1)..(780); OTHER INFORMATION: ltl7780.18-09-854-867-385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                RESULT 18
US-09-854-867-385
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                                        Sequence 730, Application US/10087192

Publication No. US20020182586A1

GENERAL INFORMATION:
APPLICANT: Moris, David W.
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT FILING DATE: 2002-03-01

PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
SOFTWARE: FESE FOR WINDOWS VERSION 4.0
SEQ ID NO 730
                                                                                                                                                                                                                                                                                                                                                                                                                          48.4%; Score 643.4; DB 13;
85.4%; Pred. No. 4.1e-188;
tive 0; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(161334)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                        al Similarity 85.4
781; Conservative
                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                               161334
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Best Local S:
Matches 781
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                                                                                                         Length 157090;
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US-10-672-764A-34/C

Sequence 34, Application US/10672764A

Sequence 34, Application US/10672764A

Publication No. US20040156832A1

GENERAL INFORMATION:

APPLICANT: Jolly, Chris

TITLE OF INVENTION: Immunoglobulin Compositions and Methods

FILE REPERENCE: 13311.1001U

CURRENT APPLICATION NUMBER: US/10/672,764A

CURRENT FILING DATE: 2003-09-26

NUMBER OF SEQ ID NOS: 68

SOFTWARE: FactSEQ for Windows Version 4.0

SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.3%; Score 601.4; DB 18;
87.0%; Pred. No. 5e-175;
iive 0; Mismatches 84; 1
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Best Local Similarity 87.0
Matches 689; Conservative
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; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-17907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17907, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CARGILL,
ATTLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT PILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SEQ ID NO 17907
LENGTH: 108773
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46.5%; Score 618; DB 19; Length 108773;

Best Local Similarity 88.8%; Pred. No. 2.8e-180;

Matches 695; Conservative 1; Mismatches 69; Indels 18;
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NAME/KEY: misc_feature
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US-10-741-600-17907
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                        DB 13; Length 180557;
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                        Score 579.8; DB 13
Pred. No. 2.9e-168;
0; Mismatches 90;
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86.0%;
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                                      Best Local Similarity 86.0
Matches 683; Conservative
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  GAAGGTGACCGCATCCATCTTTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAAT
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| Publication No. US20020119929A1
| GENERAL INFORMATION |
| APPLICANT: Bishop, Colin E. |
| APPLICANT: Byoulnik, Alexander I. |
| APPLICANT: Byoulnik, Alexander I. |
| APPLICANT: Byoulnik, Alexander I. |
| APPLICANT: Byoulnik, Alexander I. |
| APPLICANT: Byoulnik, Alexander I. |
| APPLICANT: Byoulnik, Alexander I. |
| APPLICANT: Byoulnik, Alexander I. |
| APPLICANT: Byoulnik, Alexander I. |
| TILE OF INVENTION: CAN I AND ITS ROLE IN MAMMALIAN INFERTILITY |
| FILE REFERENCE: P02066US1/10024824 |
| CURRENT APPLICATION NUMBER: US/10/003,806 |
| CURRENT FILING DATE: 2000-11-03 |
| RUMBER OF SEQ ID NOS: 14 |
| SOFTWARE: Patentin version 3.1 |
| SOFTWARE: Patentin version 3.1 |
| SEQ ID NO 6 |
| LENGTH: 180557 |
| TYPE: DNA |
| ORGANISM: Human
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                                                                                          VASCULAR DISEASE
                                                                                                                                                                                                                                                                                                                                                                                   Score 570.2; DB 15; Length.
Pred. No. 2.7e-165;
0; Mismatches 71; Indels
                                                                                                                                                            assigned
                                                                                                                                                            yet
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                                                                         TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF FILE REFERENCE: MMI-008
CURRENT APPLICATION NUMBER: US/10/017,117
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: No. US20030124535A1
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                           g
                              ; Sequence 1, Application US/10017117; Publication No. US20030124535A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature; LOCATION: (1)..(161671); CTHER INFORMATION: n = a,t,c or US-10-017-117-1
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Best Local Similarity 88.5%;
Matches 655; Conservative
                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                         LENGTH: 161671
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                                                                                                                                                                                              Score 579.8; DB 13;
Pred. No. 2.9e-168;
0; Mismatches 90;
; CURRENT APPLICATION NUMBER: US/10/003,806
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 60/245,872
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 9
; LENGTH: 180557
; TYPE: DNA
; OKGANISM: Human
US-10-003-806-9
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Best Local Similarity 86.0%;
Matches 683; Conservative
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APPLICANT: BESEME, FREDERIC
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APPLICANT: BESIME, FREDERIC
APPLICANT: BEDIN, FREDERIC
APPLICANT: PARAHGOS-BACCALA, GLAUCIA
APPLICANT: COLINTA PRADEL, FLORENCE
APPLICANT: JOLIVER: PRINARD
APPLICANT: JOLIVER: PHILIP
APPLICANT: TUKE, PHILIP
APPLICANT: TUKE, PHILIP
TITLE OF INVENTION: ASSOCIATED WITH MULITPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT
TITLE OF INVENTION: THERAPEUTIC PURPOSES
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                                       1138 GACCCACGGCTTCTAATAGAGCTATAACACTCACGCATGGCCCAAGATTCCATTGCTTG
                                                                                               GCCTGGGTTTTGTCCTAATAGAACTGAACACTGGTCACTGGGTTCCATGGTTCTTTCCAT
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,847
FILING DATE: 26-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: OLIFF & BERRIDGE, PLC P.O. BOX 19928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 102, Application US/08979847; Publication No. US20030039664A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INCRMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55376 CCCCTGGTAACA 55387
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & B
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MEDIUM TYPE: Floppy
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STRANDEDNESS:
TOPOLOGY: line
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US-08-979-847-102
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CITY: AL
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GCTGCTGACTTCCATCCCATTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGCGA 1017
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GENERAL INFORMATION:

APPLICANT: Williams, Amanda
APPLICANT: Williams, Amanda
APPLICANT: Boland, Joseph F.

APPLICANT: Boland, Joseph F.

APPLICANT: Alvarez, Chris
APPLICANT: Alvarez, Chris
APPLICANT: Wetzel, Jon C.

APPLICANT: Wetzel, Jon C.

APPLICANT: Wetzel, Jon C.

APPLICANT: Wetzel, Jon C.

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APPLICANT: Wetzel, Jon C.

APPLICANT: Wetzel, Jon C.

APPLICANT: Wetzel, Jon C.

APPLICANT: Wowell C.

PRIOR REFERENCE: 44921-5026

CURRENT APPLICATION NUMBER: US/10/240,425

CURRENT APPLICATION NUMBER: US/00-09-30

PRIOR APPLICATION NUMBER: US 60/193,446

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-03-31

NUMBER OF SEQ ID NOS: 1588

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 1102

LENGTH: 134292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 17; Length 134292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040033502A1 AL031983
US-10-240-425-1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
41.0%; Score 545.4; DB 17; Length
Best Local Similarity 85.9%; Pred. No. 1.3e-157;
Matches 680; Conservative 0; Mismatches 89; Indels
                                                                                                                                                                                                             Sequence 1102, Application US/10240425 Publication No. US20040033502A1
                                                                                                          74827 CACCGCCATCTTGGAAGCTG 74846
                                                                     CACTGCCATTTTGGTAGCGG 1282
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ORGANISM: Homo sapiens
                                                                                                                                                                             RESULT 24
US-10-240-425-1102
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Pred. No. 1e-158;
0; Mismatches 47; Indels
                                                                                                                            Version #1.30
                                                                                                                                       CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/114,104
FILING DATE: 03-Apr-2002
CLASSIFICATION NUMBER: US/10/114,104
PRIOR APPLICATION NUMBER: 08/979,847
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REFERENCE/DOCKET NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 102
                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INPORMATION:
TELEPHONE: 703-836-6400
TELEPHONE: 703-836-2787
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 635 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Local Similarity 92.4%;
les 572; Conservative
                                                         COMPUTER READABLE FORM:
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ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
THERAPEUTIC PURPOSES
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                                             Length 635;
                                                                               Indels
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                                               Score 545; DB 8;
Pred. No. 1e-158;
                                                                               0; Mismatches
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CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
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PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 102, Application US/10114104 Publication No. US20030198647A1 GENERAL INFORMATION:
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BESEME, FREDERIC
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TUKE, PHILIP
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                                             41.0%;
larity 92.4%;
Conservative
                                                               Best Local Similarity
Matches 572; Conserv
MOLECULE TYPE:
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US-10-114-104-102
 , MOLECULE TYPI
US-08-979-847-102
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; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040048253A1 LG:429446.1:2000FEB18
US-10-220-12-15
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                                                                                                                                         Gaps
                                                                                                                                         14;
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; Sequence 6792, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
                                                                                                 Score 536.2; DB 17;
Pred. No. 6.5e-156;
0; Mismatches 135;
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                                                                                                 Query Match
Best Local Similarity 81.4%;
Matches 650; Conservative
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60/184,776;
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APPLICANT: HODGSON, David M.
APPLICANT: LINCOLN, Stephen E.
APPLICANT: LINCOLN, Stephen E.
APPLICANT: LINCOLN, Stephen E.
APPLICANT: LINCOLN, Stephen E.
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/10/220,120
CURRENT APPLICATION NUMBER: 60/184,777; 60/184,797; 60/184,698; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/
Sequence 15, Application US/10220120 Publication No. US20040048253A1 GENERAL INFORMATION:
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ROSEBRRRY, Ann M.
ROSEBRRRY, Ann M.
RUSSO, Frank D.
STOCKDREHER, Theresa K.
DAFFO, Abel
WRIGHT, Rachel J.
YAP, Piterre E.
YU, Jimmy Y.
BRADLEY, Diana L.
BRADLEY, Diana L.
BRADLEY, Howard J.
CHEN, Wensheng
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APPLICANT: PANZER, SCOtt R.
APPLICANT: SPICO, Peter A.
APPLICANT: SPICO, Peter A.
APPLICANT: SHAH, Purvi
APPLICANT: CHALUP, Michael S.
APPLICANT: CHALUP, Michael S.
APPLICANT: CHANG, Simon C.
APPLICANT: CHEN, Alice
APPLICANT: D'SA, Steven A.
APPLICANT: D'SA, Steven A.
APPLICANT: D'SA, Stefan
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                                                                                          ATTANATCATGCAACTGCA 875
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GREENAWALT, Lila B.
HILLMAN, Jennifer L.
JONES, Anissa L.
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LENGTH: 849
TYPE: DNA
ORGANISM: Homo sapiens
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ATCCCCCAGTAACA 1329
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LOCATION: (1)...(80032
                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: misc feature
LOCATION: (1)...(366710)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17727, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001496
CURRENT APPLICATION NUMBER: US/10/719, 993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARES PARESEQ for Windows Version 4.0
SEQ ID NO 6792
LENGTH: 366710
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39.9%; Score 530.6; DB 18;
Best Local Similarity 91.0%; Pred. No. 9.4e-153;
Matches 563; Conservative 0; Mismatches 56;
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                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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US-10-741-600-17727/c
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                                                                                                                                                                                                                                                                                         Length 80032;
                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                         38.7%; Score 513.8; DB 19; Length 83.0%; Pred. No. 7.2e-148; ive 3; Mismatches 108; Indels
FILE REFERENCE: CL001449
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17727
LENGTH: 80032
                                                                                                                                                                                                         LOCATION: (1) ... (80032)
COTHER INFORMATION: n = A,T,C or G, US-10-741-600-17727
                                                                                                                                                                                                                                                                                                                Best Local Similarity 83.0
Matches 659; Conservative
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170582 CATCGGCCATCCTCCCCAACAGACTTTGGGTTTTCCTGTTGAGAGGGGGTACTCAGAGAC 170523
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1198 GTATCTGTGAGGCCAAGAACCCCAGGTCAGAGAANGTGAGGCTTGCCACCATTGGGGAAG 1257
                                                                                                                                                                                                 Sequence 3. Application US/09731231A
; Sequence 3. Application US/09731231A
; Patent No. US20020082189A1
; GENERAL INFORMATION:
; APPLICANT GUGGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLOOLOGO
; CURRENT APPLICATION NUMBER: US/09/731,231A
; CURRENT APPLICATION NUMBER: US/09/731,231A
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FaatSEQ for Windows Version 4.0
; SOFTWARE: PackEQ for Windows Version 4.0
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Pred. No. 7.3e-144;
0; Mismatches 62;
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NAME/KEY: misc feature

LOCATION: (1)...(326014)

OTHER INFORMATION: n = A,T,C or
US-09-731-231A-3
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Best Local Similarity 88.7%;
Matches 557; Conservative
                                                                                                                    5783
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ORGANISM: Human
                                                                                                                    5787 TGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
38.5%; Score 512; DB 17; Length 17758;
Best Local Similarity 84.7%; Pred. No. 1.2e-147;
Matches 614; Conservative 0; Mismatches 93; Indels 18;
                                                                                                31061 ACCCGCCAGTAACA 31048
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
CORGANISM: Homo sapiens
US-10-264-237-2833
                                                                        RESULT 30
US-10-264-237-2833/c
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                                                                  TITCACICIAITAAAICAIGCAACIGCA 875
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                                                                                                                                               Sequence 3, Application US/10751985
Sequence 3, Application US/10751985
Publication No. US20040126861A1
GENERAL INFORMATION:
APPLICANT: GENGLER. Karl et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REPERENCE: CLOO1007CON
CURRENT APPLICATION NUMBER: US/10/751,985
CURRENT FILING DATE: 2004-01-07
NUMBER OF SEC ID NOS: 6
SOFTWARE: FRANKE FRANKES FOR MINDOWS VERBION 4.0
SEQ ID NO 3
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Pred. No. 7.3e-144;
0; Mismatches 62;
                                                                                  170222 Tricacrerarraaarerrecaacacca 170195
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Best Local Similarity 88.7%;
Matches 557; Conservative
                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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NAME/KEY: misc_feature LOCATION: (1)...(283351) JOTHE INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1 US-10-719-993-7065 Sequence 7065, Application US/10719993

Sequence 7065, Application US/10719993

Publication No. US2004026849A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REPRENCE: CLO01496

CURRENT APPLICATION NUMBER: US/10/719,993

CURRENT FILING DATE: 2003-11-24

NUMBER OF SEQ ID NOS: 55342

SEQ ID NO 7065

LENGTH: 283351

LENGTH: 283351 175340 175044 175220 174984 642 2, 174985 Argccccaatrcagcaggaagcrgtragagcagrcatrggccaaccrcccaacagc 174805 GTTTGTCTTCCAGAATTGAAACTGTAAAACTACAAATGGTTCTTCAAATGGAGCCCCA 175281 AGGATATAAACCCAGGCATTCGAGCTGGCAACGGCAACCCCCTTTGGGTCCCCTTC 283 GTTTGTCTTCCAGAATTGAAGCTGTAAAGCTACAAATAGTTCTTCAAATGGAACCCCA CAACTTAGCTCACACCCGACCAATCAGAGGCTCACTAAAATGCTAATCAGGCAAAAACA GGAGGTAAAGCAATAGCCAATCATCTATTGCCTGAGAGCACAGGGAAGGACAAGGATT 763 GGGATATAAACTCCAGGCATTCAAGCCAGCAACAGCAACCCCCTTTGGGTCCCCTTCCCATT 343 GATGCAGTCCATGACTAAAATCTACCGTGGACCCCTGGACCGGCCTGCTAGACTATGCTC 403 IGAIGITAAIGACATIGAAGICACCCCICCCGAGGAAAICICAACIGCACAACCCCIACI 463 ACACTCCAATTCAGTAGGAAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACT CTAAGAATCCCNAAGCCTANCTGGGAAGGTGACCGCATCCATCTTAAACATGGGGCTTG Gaps Query Match
36.0%; Score 478.6; DB 18; Length 283351;
Best Local Similarity 90.1%; Pred. No. 1.3e-136;
Matches 534; Conservative 1; Mismatches 52; Indels 6; G

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Query Match
Best Local Similarity 90.1
Matches 534; Conservative
                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
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US-10-741-600-17676
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1 LOCATION: (1)...(283351)

2 OTHER TOORWATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-

US-10-741-600-17995
                                                                                                                      APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17995
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Pred. No. 1.3e-136;
1; Mismatches 52; Indels
                                                                                   ; sequence 17995, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
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Best Local Similarity 90.1%;
Matches 534; Conservative
                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism US-10-719-993-6815
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                                                                                            ASSOCIATED WITH METHODS OF DETECTION AND
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; Sequence 6815, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INPORMATION:
    APPLICANT: CREGILL, Michele et al.
    APPLICANT: CREGILL, Michele et al.
    TITLE OF INVENTION: ALZHEIMER'S DISEASE, MET
    FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FRAELSEQ for Windows Version 4.0
; SEQ ID NO 6815
; LENGTH: 1980090
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; Publication No. US20050026169A1
; Pablication Ro. US2050026169A1
; APPLICANT: CARGILL, Michele et al.
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LOCATION: (1). ... (1980090)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 17676
LENGTH: 1980090
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Sequence 678, Application US/10276774

Publication No. US20040053245A1

GENERAL INFORMATION:

APPLICANT: Hyeeq, Inc.

APPLICANT: Tang, Y, Tom et al

TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides

FILE REPERENCE: 21272-030

CURRENT APPLICATION NUMBER: US/10/276,774

CURRENT FILING DATE: 2002-11-18
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                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 28, Application US/10632793
Sequence 28, Application No. US20040048298A1
Sequence 28, Application No. US20040048298A1
GENERAL INFORMATION:
APPLICANT: PARANHOS-BACCALA, Glaucia
APPLICANT: PARANHOS-BACCALA, Glaucia
TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH P
TITLE OF INVENTION: ENDOGENEOUS DISEASE, LABELING METHOD AND REAGENT
FILE REFERENCE: 110048
CURRENT APPLICATION NUMBER: US/10/632,793
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                                                                                                                                                                                                                                                     Score 468.8; DB 17;
Pred. No. 1.1e-134;
0; Mismatches 59;
Query Match 35.3%;
Best Local Similarity 88.5%;
Matches 533; Conservative
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US-10-276-774-678
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PRIOR APPLICATION NUMBER: US 09/
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
SOFTWARE: PatentIn version 3.1
SEQ ID NO 148
LENGTH: 22436
                                                                                                                                    Query Match 35.0%;
Best Local Similarity 88.8%;
Matches 539; Conservative
                                                                                             ORGANISM: Homo Bapiens
US-09-997-722-148
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US-10-087-192-1666
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US-09-97-722-148
US-09-997-722-148
Sequence 140, Application US/09997722
Sequence 140, Application US/09997722
Sequence 140, Application US/09997722
Sequence 140, Application No. US20040072154A1
TEREPERATION:
TILE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
TILE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2001-11-30
PRIOR FILING DATE: 2000-12-22
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                                                                                                                                                                                                         Length 3372;
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Pred. No. 2.2e-133;
0; Mismatches 57;
        CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US/09/869,927
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: PCT/FR00/00144
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 1999-01-21
NUMBER OF SEQ ID NOS: 33
SOSTWARE: Patentin version 3.1
SEQ ID NO 28
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89.7%;
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                                                                                                                                                                                                                                       Matches 498; Conservative
                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
US-10-632-793-28
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; Sequence 1666, Application No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Engelhard, Eric K.
; TILLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 5.2945.200012.2
; CURRENT APPLICATION NUMBER: US/10/087, 192
; CURRENT APPLICATION NUMBER: US/000203-01.
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-13-01
; PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                         57;
                                                                                                                                                                                                 DB 11;
                                                                                                                                                                                                 Score 465; DB 11,
Pred. No. 6e-133;
0; Mismatches 5
09/198,586
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280025 GCCGGCAGTGCCTACCCGCTTTGGGTCCCCTCTGTTTGTATGGGAGCTCTGTTTTCACTC 280084
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PRIOR APPLICATION NUMBER: US 09/798,586

PRIOR FILING DATE: 2001-03-02

NUMBER OF EGG ID NOS: 2059

SCOTTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1666

LENGTH: 285020

TYPE: DNA

ORGANISM: Homo sapien8
                                                                                                       | FEATURE:
| NAME/KEY: misc_feature
| LOCATION: (1) ... (285020)
| OTHER INFORMATION: n = A,T,C or G
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Search completed: February 21, 2005, 19:18:30 Job_time : 750.518 secs

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Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Database

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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
18t strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMV8PORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full.length cDNA libraries and normalization
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Pred. No. 1.2e-202;
0; Mismatches 69;
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/plasmid="pcMvSPORT_6"
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Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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CR617248.1 GI:50498055
HTC; CNSLT_CDNA.
Homo sapiens (human)
HOMO sapiens (human)
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 2749)
Sukaryota (brimata)
Full-length cDNA libraries and normalization
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Qy 661 ACCAATCAGAGAGTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCC 720 Db 2564 ACCAATCAGAGAGCTCACTAAAATGCTAATTAGGCAAAGAGGGTAAAAGAAATAGCC 2623 Qy 721 AATCATCTATTGCCTGAGAGCACAGGAACGAACGAATTGGGATATAAACTCAGGA 780 Db 2624 AATCATCTATTGCCTGAGAGCACAGGAGGACAATGATCGGGATATAAACCCAAGT 2683 Qy 781 TTCAAGCCAGCAACCACCATTGGGTCCCCTCCATTGTATGAGAGCTCTGTTT 840 Db 2684 TTCAAGCCAGCAACGACACCCCTTTGGGTCCCTCCCATTGTATGAGGGCTCTGTTT 2743	Oy 841 CACTCT 846 Db 2744 CATGCT 2749	RESULT 3 CR622175 CR622175 CR622175 CR622175 CR622175 DEFINITION full-length cDNA clone CS0D1051YM13 of Placenta Cot 25-normalized ACCESSION CR622175 VERSION CR622175 VERSION CR622175.1 G1:50502982 KEYWORDS HTC; CNSLT_CDNA. SOURCE SO	DEGRANSIAN CONTROL SEQUENCE OF CONTROL OF CO	Faraday Avenue C (bases 1 to 2500) AUTHORS Genoscope. TITLE Direct Submission JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) COMMENT 1st strand CDNA was primed with a NotI-oligo(dT) primer. Five prime	of the pCMVSPORT 6 vectorization by Life Technolo	<pre>ganism="Homo sapiens" 1_type="mRN" -xref="taxon:9606" one="cS0D1051YM13" ssue_type="Placenta Cot 25-normalizeramid="pcMVSPORT_6"</pre>	Query Match 52.8*; Score 702; DB 3; Length 2500; Best Local Similarity 90.6*; Pred. No. 3.2e-201; Indels 12; Gaps 1; Matches 763; Conservative 0; Mismatches 67; Incanantary Qy Incanantary Indels 12; Gaps 1; Db 1669 TCAAAATCGAGAGCTTTAGACTTGCTAACCGCTGAAAGGGGGAACCTGTTATTTT 1728	Qy 61 AGGGAAGAATGCTGTTAGTATGTTAATCAATCTGGAATGATTACTGAGAAAGTTAAAGA 120 Db 1729 AGGGAAGAATGCTGTTATTATGTTAATCAATCCGCAATCGTCACTCAC

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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRX cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                             X365066 1000 apiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA COT CS-NORMALIZED Homo sapiens CDNA LONE CSODI046YA18 3-PRIME, mRNA sequence.
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Corganism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSOD1046YN18"

/tlssue type="PLACENTA COT 25-NORMALIZED"

/clone="lb="taxon sapiens PLACENTA COT 25-NORMALIZED"

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/note="lst strand cDNA was primed with a NotI-oligo(dT)

/note="lst prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and ECOR V

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                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
11, W.B.; Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Dmpublished (2001)
On May 5, 2003 this sequence version replaced gi:30374869.
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3; Mismatches 69;
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- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Pred. No. 2.7e-200;
0; Mismatches 67;
                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI044XK0"
/tissue_type="Placenta Cot 25"
/plasmid="pcMVSPORT_6"
                                                                                                                                   Location/Qualifiers
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larity 90.6%;
Conservative 0
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BX337769 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODIO51YM13 3-PRIME, mRNA sequence.
BX337769.2 GI:46272079
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                                                                     Gaps
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                             Léngth
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                               DB 3;
                                 Score 678.6; DB 3;
Pred. No. 4.3e-194;
                                                                       0; Mismatches
                                 51.1%;
90.5%;
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                                                     Similarity
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191 9100 GENYZ cedex - FRANCE (B-mail : seqref@genoscope.cns.fr |
192 191 9100 GENYZ cedex - FRANCE (B-mail : seqref@genoscope.cns.fr |
193 191 9100 GENYZ cedex - FRANCE (B-mail : seqref@genoscope.cns.fr |
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full-length cDNA clone CS0DE013YI20 of Placenta of Homo sapiens
(human).
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Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

11 (bases 1 to 2716)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished
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                                     361 AATCTACCGTGGACCCTGGACCGGCCTGCTAGACTATGCTCTGATGTTAATGACATTGA
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="CSODE013Y120"
/tissue_type="Placenta"
/plasmid="pCMVSPORT_6"
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/db_xref="taxon:9606"
   CGAAGCTGTAAAACTA-----
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequencecope.cns.fr, Web : www.genoscope.cns.fr
End cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1058 bp mRNA linear EST 23-APR-2004
BX378303 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
Clone CSODI018YH07 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNa was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Li (Bases 1 to 1058)
Li, W. B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Ompublished (2001)
On May 8, 2003 this sequence version replaced gi:30439129.
Contact: Genoscope
                                                                                                                          188
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                                                                                                      780 ATTCAAGCCAGCAACAGCAACCCCCTTTGGGTCCCCTCCCATT--GTATGGGAGCTCTGT
AGGGTGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCC
                         TANCTEGGAAGGTGACCGCATCCATCTTAAACATGGGGCTTGCAACTTAGCTCACACCC
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Pred. No. 6.2e-189;
1; Mismatches 92;
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/db_xref="taxon:9606"
/clone="CS0DI018YH07"
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Matches 727; Conservative
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqreté@enoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
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into the Not I and EcoR V sites of the pCMVSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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          Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue types"PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="list strand cDNA was primed with a Not1-oligo(dT)
primer. Five plane end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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                              Catarrhin; Hominidae; Homo.
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                              Manualia; Butheria; Primates; Catarrhini; Homin
1 (bases 1 to 998)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 2, 2003 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , 669.4; DB 5; L
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/db_xref="taxon:9606"
/clone="CS0DI051YM13"
               Chordata;
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Contact: Genoscope Genoscope - Centre National de Sequencage Z rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: segrefégenoscope.cns.fr, Web.: www.genoscope.cns.fr Email: segrefégenoscope.cns.fr, Web.: www.genoscope.cns.fr Ist strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecory sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4215.r For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODE012DE12NP1&c=4215.r. For more information about Lis cluster, see http://www.genoscope.cns.fr/cdna?s=CSODE012DE12NP1&c=4215.r. Location/Qualifiers 1.1019 /mol type="mRNA" /mol type="mRNA" /done="Vector: PCNVSPORF 6; 1st strand cDNA was primed /note="Vector: pCNVSPORF 6; 1st strand cDNA was primed /note="Vector: pCNVSPORF 6; 1st strand cDNA was primed /note="Vector: pCNVSPORF 6; 1st strand cDNA was primed /note="Vector: pCNVSPORF 6; 1st strand cDNA was primed /note="Vector: pCNVSPORF 6; 1st strand cDNA was primed /note="Vector: pCNVSPORF 6; 1st strand cDNA was primed /note="Vector: pCNVSPORF 6; 1st strand cDNA was primed /note="Vector: pCNVSPORF 6; 1st strand cDNA was not normalized." Library was not normalized." Library was not normalized."	Query Match 49.1%; Score 652.2; DB 5; Length 1019; Best Local Similarity 85.5%; Pred. No. 3.3e-186; Matches 725; Conservative 19; Mismatches 91; Indels 13; Gaps 1 TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAGAGGGGGAACCTGTTTATTTTT 835 TCAAAATCGAAGAGCTTTAGACTTGCTAACGGCAAAGAGGGGGAACCTGTTTATTTTTTTT		OY 241 TITACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTCTCTTCCAGAAT 300	·• ,
	TAGG 	Oy 541 GGGTGGACTGAGACTAGGTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCT 600 Db 304 TGGGGGACTGAGACAGGACTAGCTGGATTTCYTAGGTGACTAAGAATCCCTAAGGTCT 245 Oy 601 ANCTGGGAAGGTGACCACCTTTTAAACAGGGGCTTGCAACTAAGCTCACCCG 600 Db 244 AGCTGGAAGGTGACCACCTTTTAAACACGGGGCTTGCAACTTAGCTCACACCTG 185 Oy 661 ACCAATCAGAGGCTCACTAAAACACTAATCAGGCAAAAAACACGGAGGTAAAGCCACCTG 185 Db 184 ACCAATCAGAGGCTCACTAAAATGCTAATCAGGCAAAAAACAGGAGGTAAAGCAATAGCC 720 Db 184 ACCAATCAGAGAGCTCACTAAAAATGCTAAACAGAGAAAAAAAGAGAAATAGCC 720 Db 184 ACCAATCAGAGAGCTCACTAAAATGCTAAACTAGGCAAAAAAAGAGAAATAGCC 720	Oy 721 AATCATCTATTGCCTGAGAGCACAGGGAAGGACAAGGATTGGGATATAAACTCAGGCA 780 Db 124 AATCATCTATTGCCTGAGGAGCACAGGAGGACAATGATGGATATAAACCCAAGTC 65 Oy 781 TTCAAGCCAGCAACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGAGCTCTGTTTT 840 Db 64 TTCGAGGCGGCAACGGCAACCCCNNTNNTGGTNNCNNTGGCGTTTGTGTGGAGTTTTGTTT 5	RESULT 9 BX439636/C LOCUS BX439636 BX43000000000000000000000000000000000000

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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequencope.cns.fr, Web : www.genoscope.cns.fr
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end enriched, double-strand cDNA was digested with Not I and cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BX357208 BX357208 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI022XJ18 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                               TGAAGCTGTAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA 360
                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 758)
1. (bases 1 to 758)
1. W. B., Gruber, C., Jessee, J. and Polayes, D. Pull-length cDNA libraries and normalization (Dupblished (2001))
On May 5, 2003 this sequence version replaced gi:30376125.
Contact: Genoscope
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         AATTTGAGATCGAATATAATGTAGAGCAGAGGACCTTCAAAACACTGCACCCTGGGGCCTT
                                                                                               CCTCAGCCAATGGATGCCCTGGACTCCCCTTCTTAGGACCTCTAGCAGCTATAATATT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

11 (bases 1 to 966)

12 (bases 1 to 966)

13 (bases 1 to 966)

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/clone="Tissue type="PLACENTA COT 25-NORWALIZED"
/clone="list strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was primer and cDNA was grimed with a NotI-oligo dT)
sprimer: Five prime end enriched, double-strand cDNA was sprimed with Not I and cloned into the Not I and EcoR values of the pCMVSPORT 6 vector. Library was normalized.
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82.5%; Pred. No. 2.2e-173;
tive 24; Mismatches 110; Indels
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BI087886 771 bp mRNA linear EST 20-JUN-2001
602852690F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4993894 5',
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                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
Plate: LLAM11015 row
High quality sequence stop: 762.
High quality sequence stop: 762.
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                   16
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/clone_lib="NIH_MGC_10"
                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                         /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CSOID2XV18"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone=lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TA------CAAATGGAGCCCAAGATGCAGTCCAAGACTAAGATCTACCGCAGAC
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                                                                          For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODI022DE09NP1&c=4215.r. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                 Length 758;
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                                                                                                                                                                                                                                                                                                                                                 45.8%; Score 608.2; DB 5.88.1%; Pred. No. 7.2e-173.ive 9; Mismatches 69
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TCCCCTCCCATTGTATGGGAGCTCTGTTTTCACTCTATTTCACTCATGCAA 870
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shirs
TOSHIVIKI and Piero Carninci (RIKEN)
TOSHIVIKI and Piero Carninci (RIKEN)
TOSHIVIKI Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadam@systemsbiology.org
contact: amadam@systemsbiology.org
Anup Madan, Jessica Pahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1124 TTGCAATTTAGCTCACCACCCGACCAATCAGGTAGTAAAGAGAGCTCACTAAAATGCTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGGCAAAACAGAGGTAAAGCAATAGCCAATCATCTATTGCCTGAGAGCACAGGGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       520 ACTIGGGITTTCCTGTTGAGAGGGTGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 4204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5565109"
/tissuc_type="Brain, hippocampus"
/clone_lib="NH MGC_95"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

44.5%; Score 592; DB 3;
Best Local Similarity 81.1%; Pred. No. 1e-167;
Matches 755; Conservative 0; Mismatches 128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab host="DH10B"
/note="Vector: pBluescript"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BC035153 4204 bp mRNA linear HTC 19-NOV-2003
Homo sapiens hypothetical protein FLJ22313, mRNA (cDNA clone
MAMOE:5565109), with apparent retained intron.
                                                                                                                                                                                                                                                                                         705
                                                                                                                                                                                                                                                                                                                                                                                                                  647
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Submitted (31-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
                                                                    CCCAATTCAGCAGGAAGCAGTTAGAGCGGTCGTC-GGCAACCTCCCCAAAAGCACTTAGG
                                                                                                                                                                                                                                    648 ĠĂTĂTTĂACCĂAĞTCTTCGAĞCGGCAACGGCAACCCCCTTTGGGTCCCCTCTTTGT
                                       TCCAATTCAGTAGGAAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGG
                                                                                                                                                                                                        AGAATCCCNAAGCCTANCTGGGAAGGTGACCGCATCCATCTTTAAACATGGGGCTTGCAA
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     825 ATGGGAGCTCTGTTTTCACTCTATTTCACTCTATTAAATCATGCAACTGCA
                                                                                                                    TTTTCCTGT-TGAGAGGGTGGACTGAGAGACAGGACTAGCTGGATTT
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Homo sapiens
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155 CTTCAAAACACTGCACCTGGGGCCTCCTCAGCCAATGGATGCCTGGACTCTCCCCTTC 214 61 [335 GAACCCCAGAIGCAGICCAIGACTAAAAICTACCGIGGACCCCIGGACCGGCTGCIAGA 394	CCCCACGATCTGATGATATGACATCAAAGGCACCCCTCCTGAGGAAATCTCAGCTGCACAA CCCCTACTACACACCACATTCAGTAGGAAGGCACTTTAGAGCAGTTGTCAGCCAACCTCCCCA	515 ACAGTACTTGGGTTTCCTGTTGAGAGGTGAGAGACAGGACTAGCTGGATTTCC 574	635 GGGGCTTGCAACTTAGCTCACCCGACCAATCAGAGGCTCACTAAAATGCTAATCAGG 694	755 755 611	SULT 15 SULT 15 459153/c EX459153 EX459153 FINITION BX459153 CESSION BX459153 CESSION BX459153 CESSION BX459153 CESSION BX459153 CESSION BX459153 CESSION BX459153 CESSION BX459153 CESSION BX459153 CESSION BX459153 CESSION BX459153 CESSION BX459153 CESSION BX459153 CESSION BX459153	EST. Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebx Mammalia; Euthebria; Primates; Catarrhini; Homir 1 (bases 1 to 900) Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length CDNA libraries and normalization from,blished (2001)	
6 6 6 6 6	8 8 8	2 8 8 8	8 8 8	8 6 6	S A S	RESUL RESUL BX459 LOCUS DEFIN ACCES	KEY SOU O O REF T	S W
Qy 991 GTGTCCACTGTGTCCTGATCCAGCGAGGTACCCATTGCCACTCCGATCAGGCTAAAGG 1050 Db 1465	1171 CCGCATGGCCCAAGATTCCATTCCTTGGTATCTGTGAGGCCAAGAACCCCAGGTC	Oy 1231 ANGTGAGGTTGCCACTTGGGAAGTGGCCCACTGCCACTGGGGCCCACCACCACCACCACCACCACCACCACCACCACC	RESULT 14 CN272394 CN272394 CN272394 CN272394 CN272394 CN272394 CN272394 CN272394 CN272394 CN272394 CN272394.1 GI:47288808	KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens CRAATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmalia; Butheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 719) AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Marage, J., Fisk, G.J.,	LIJIA AND TO THE TEACH TO THE TEACH TO THE TEACH TO THE TEACH TO THE TOTAL THE TEACH TO THE TEAC	Regenerative Medicine Geron Corporation 230 Constitution Drive, Menlo Park, CA 94025, USA 230 Constitution Drive, Menlo Park, CA 94025, USA Tel: 650 473 8658 Fax: 650 473 760 Email: rbrandenberger@geron.com Insert Length: 719 Std Error: 0.00. FEATURES Location/Qualifiers 10.719 crandism="Homo sapiens" /mol Lype="Homo sapiens" /mol Lype="MRNA" /m	/ Lissue Lype="embryonic stem cell, retinoic acid and mitogen-treated hES cell line H7" / clone_lib="GRN_PREME"	Query Match 42.2%; Score 561; DB 7; Length 719; Best Local Similarity 85.4%; Pred. No. 1.6e-158; Matches 657; Conservative 0; Mismatches 62; Indels 50; Gaps 1; Qy 95 GGAATCATTACTGAGAAAGTTAAAGAAATTTGAGATCGAATAAATGTAGAGGAGGAC 154 Db 1 GGAATCGTCACTGAGAAAGTTAAAGAAATTCGAGATCGAATACAAGGAGGAGGAGGGG 60

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/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB;
cDNA-collection"
96 MVCCATSCACTGCCTGAGAGCACRGCAGGAGGAGACVATGMGCGGGAGRTAAASCCAAGTC 37
                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1002)
Ansorge, W., Krieger, S., Regiert, T., Rittmueller, C., Schwager, B., Mewes, H.W., Well, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the
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Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germanny) within the CDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         German Genome Project.

No s1 sequence available.
This clone (DKFZp781M064) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
Location/Qualifiers
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Pred. No. 4e-140;
0; Mismatches 72;
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                                                               781 TTCAAGCCAGGAACAGCAACCCCTTTGGGTCCC
36 BCCGCGCGGGCTACGGCKCCCCCTKTGGTCCCC
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dclone="NKRZPYB1M064"
/dev_stage="adult"
/lab_host="DH108"
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87.68;
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/cissue type="PlACENTA"
/cone lib="Homo saptens PLACENTA"
/note="Vector: PCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
with a NotI-oligo(dT) primer. Five prime end enriched,
with a NotI constand cDNA was digested with Not I and cloned into
the Not I and ECORV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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             normalized. Library was constructed by Life Technologies,
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               was not normalized. Lizer.

division of invitrogen.

This sequence belongs to sequence cluster 4215.r

This sequence belongs to sequence cluster, see

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CSODE013BE10NP1&c=4215.r.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 900;
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Larity 77.5%; Pred. No. 2.5e-153;
Conservative 49; Mismatches 120; Indels
                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE013Y120"
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AGENCOURT_6708649 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5747240
5', mRNA sequence.
BM918330.1 GI:19368709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens butaroa; Chordata; Craniata; Vertebrata; Buteleostomi; Butheria; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 999) thtp://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                                                                                                                          619;
                                                             /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
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                                                                                                                          Score 480.8; DB 9;
Pred. No. 3.7e-134;
0; Mismatches 83;
                                                                                                                                                           0; Mismatches
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-120G11.R"
                                                                                                                           36.2%;
ilarity 86.7%;
Conservative
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                                              /sex="male"
                                                                                                                                          Similarity
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Best Local Simil
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Direct Submission
Submitted (Oz-Mug-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-445-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AG113694 679 bp DNA linear GSS 03-NOV-2001
Pan troglodytes DNA, clone: PTB-120G11.R, genomic survey sequence.
AG113694
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                   513 TACATTCTTCCGGATCCAGCAGGTGTCCACTGTGCTCCTGATCCAGCGAGGCACCCCTT
                                                                                                                                                                                                                                                              333 ACTICTAATAGAGCTGTAACACT----GCATGGCCCCAAGATTCCGTTCCTTAGAATCCGT
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                                                                                                                GAGCITITIGITICGCCATCCACCACTGTT-TGCCACCGTCACAGACCCGCTGCTGACT
                                                   TTCACTCTATTAAATCATGCACTGCACTCTTCTGGTCCGTGTTTTTTATGGCTCAAGCT
                                                                                  633 rrcacacrarraaarcrrcaaacrecacrcrrcregrrcererrerrarracrecregaecr
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BAC end sequences of Library PTB
Unpublished
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R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
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Pan troglodytes
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GSS.
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AG113694/c
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Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Tokijyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Toyoda, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Tol. Subhiro-chou, Fsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mall:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                           1253
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                                                                                                                                                                                                                                                                                      GSS 04-NOV-2001
                                                                                                            CTTGGAATCCGTGGGGCCAAGAACCCCAGGTCAGAGAACGAGAGGCTTGCTGCCATCTTG 168
                                                                                                                                                                                                                                                                        AG114524 683 bp DNA linear GSS 04-NOV-200
Pan troglodytes DNA, clone: PTB-147110.R, genomic survey sequence.
AG114524
                                                                                                                                                                                                                                                                                                                                                                                                          Pan troglodytes
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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                           CTTGGTATCTGTGAGGCCAAGAACCCCAGGTCAGAGAANGTGAGGCTTGCCACCATTTGG
   CCATGACCCACGCCTTCTAATAGAGCTATAACACTCACCGCATGGCCCAAGATTCCATTC
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/clone_lib="PTB Chimpanzee Male BAC Library"
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35.8%; Score 475.2; DB 9;
al Similarity 89.6%; Pred. No. 1.8e-132;
554; Conservative 0; Mismatches 60;
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/organism="Pan troglodytes"
/mol type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-147110.R"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fujiyama, A., Hattori, M., Toyoda, A.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                                                        1254 GAAGTGGCCACTGCCATTTTGGTAGC 1280
                                                                                                                                                                                             GAAGCAACCGCCACCATGTTGGGAGC 141
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R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
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GSS.
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             Email: capbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can lettp://image.llh.gov
http://image.llh.gov
Plate: LLAMI2773 row: b column: 09
High quality sequence stop: 685.
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                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TMAGE:5747240"
/lab_host="DH108"
Strausberg, Ph.D.
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Totoki, Y., Watanabe, H. and Sakaki, Y.
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Pan troglodytes DNA, clone: PTB-030D19.F, genomic survey sequence.
AG049953
178 GCCAGCAACGGCAACCCCCTTTGGGT-CCCTCCCCTTGTATGGGAGCTCTGTTTTCACTC 236
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                               TATTICACTCTATTAAATCATGCAACTGCACTCTTCTGGTCCGTGTTTTTTATGGCTCAA
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                                                                                                                                   GCTGAGCTTTTGTTCGCCATCCACCACTGCTG-TTTGCCACCGTCACAGACCCGCTGCTG
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                                                                 Taylor, T.D., Yada, T.
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/mol_type="genomic DNA"
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R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
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Pan troglodytes
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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                                                                                                                                                                                            12;
                                       /eex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                Length 669;
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                                                                                                                                                  Score 474; DB 9; I
Pred. No. 4.2e-132;
0; Mismatches 71;
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TotoKi,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         639 ACCATTTTGGAAGCAGCCGGCCACCATGTTG
'db_xref="taxon:9598"
                    clone="PTB-030D19.F"
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Pan troglodytes
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                                                                                                                                                     35.7%;
Similarity 86.8%;
18; Conservative
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Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Direct Submission
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, WR:http://hgp.gsc.riken.go.jp/, Tel:91-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                             GSS 03-NOV-2001
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Pan troglodytes DNA, clone: PTB-097K23.F, genomic survey sequence.
                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
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Pred. No. 9.4e-131;
0; Mismatches 65;
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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Pan troglodytes
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ilarity 85.1%;
Conservative 0
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R.Site 1
R.Site 2
                 Similarity
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Matches 56
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SOURCE
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VERSION
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AUTHORS
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission
Submitted (02-AUG-2001) Asso Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel.81-45-503-911, Fax:81-45-503-911,
Tel.81-45-503-911, Fax:81-45-503-9110)

Clones are derived from the chimpanaee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
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                                                                                                                                                                                                                                                                                                                                                                                       /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db xref="taxon:9598"
/clone="PTB-124K18.F"
/sex="malle"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
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R.Site 1 : SacI
R.Site 2 : SacI.
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AGENCOURT_7917208 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6161436
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                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRL Plate: 41 Row: m Column: 10
This clone has the following problem: retained intron.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 468.2; DB 3;
Pred. No. 2.9e-130;
0; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
mol_type="mana"
/db_xref="texon:9606"
/clone="IMAGE:4724433"
/tissue_type="placenta"
/clone_lib="NIH MGC_79"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pDNR-LIB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.2%;
milarity 90.1%;
Conservative 0
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Best Local Similarity
Matches 500; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1160)
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                                                                                                                                                                                                                                        425 GCTCCCGATCGGGCTAAAGGCTTGCCATTGTTCCTGCACGGCTAAGTGCCTGGGTTCGTC
                                                                                                                                                                                                              CTAATAGAACTGAACACTGGTCACTGGGTTCCATGGTTCTCTTCCATGACCCACGGCTTC
                                                                                                                                                                                                                                                                                                                 TAATAGAGCTATAACACTCACCGCATGGCCCAAGATTCCATTCCTTGGTATCTGTGAGGC
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                                                                                                             1031 ACTCCCGATCAGGCTAAAGGCTTGCCATTGTTCCTGCCAAGGCTAAGTGCCTGGGTTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC030968 1160 bp mRNA linear HTC 19-NO<sup>N</sup>
Homo sapiens cDNA clone IMAGE:4724433, with apparent retained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAGAACCCCAGGTCAGAGAACACGAGACT
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Homo sapiens
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BC030968
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AUTHORS
TITLE
JOURNAL
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AUTHORS
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KEYWORDS
SOURCE
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BC030968
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COMMENT
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1116

1056

800

740

620

876

816

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1116

1296

GSS 03-NOV-2001

624

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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mall:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
TT-1:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                  1177 GGCCCAAGATTCCATTCCTTGGTATCTGTGAGGCCAAGAACCCCCAGGTCAGAANGTGA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 669 GAGAGCTCACTAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCCAATCATCT 728
                                                                                                                                                                                                                                                                                  AG072852 670 bp DNA linear GSS 03-NOV-200
Pan troglodytes DNA, clone: PTB-064H14.R, genomic survey sequence.
AG072852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryot̃a; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
ATTGTTCCTGCATGGCTAAGTGCCTGGGTTTGTCCTAATAGAACTGAACACTGGTCACTG
                          GGTTCCATGGTTCTTTCCATGACCCACGGCTTCTAATAGAGCTATAACACTCACCGCAT
                                                                                                                                                                                               1237 GGCTTGCCACTTTGGGAAGTGGCCCACTGCCATTTTGGTAGCGGCCCACCACCATCTT
                                                                                                        50S GGTICCACGATTCTCTTCCATGACCCACAGCTTCTAATAGAGCTATAACACTCGCCGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujjyama,A., Hattbri,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

34.3%; Score 456.2; DB 9; Length 670;

Best Local Similarity 86.4%; Pred. No. 1.1e-126;

Matches 529; Conservative 0; Mismatches 74; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .670
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-064H14.R"
                                                                                                                                                                                                                                                                                                                                              1297 GGGAGCTGTGGGAGCAAGGATCCCC 1321
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
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KEYWORDS
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AG072852
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AUTHORS
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REFERENCE
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JOURNAL
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/mol type="mRNA"
/db _xref="taxon:9606"
/db _wref="taxon:9606"
/clone="TMAGE:661436"
/tissue type="melanotic melanoma"
/tissue type="melanotic melanoma"
/lab host="DH108 (phage-resistant)"
/clone lib="NXH MGC 72"
/note="crgan: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
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                                                                                                                                                                                                                                                              Email: cgapbe-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM13513 row: 1 column: 13
High quality sequence stop: 650.
Location/Qualifiers
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                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 893)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 CCCTITGTATGGAAGCICTGTITTCACTCTATTAAATCTIGCAATTGCA------CAC
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                                                                                                                                                                                  NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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5', mRNA sequence.
BQ437925
BQ437925.1 GI:21177001
                                                                              Homo sapiens (human)
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               ACCESSION
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Pan troglodytes DNA, clone: PTB-130M15.F, genomic survey sequence. AG121669
AG121669.1 GI:16650834
GSS.
                                                                                                                                                                                                                                                                                                                                                                          284
                                                                                                                                                                                                                                                                                                            107 GAGCTCACTAAAATGCTAATTA-GCAAAAACAGGAGGTAAAGAAATAGCCAATCATCTT
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                                                                                                                                                                                                                                                                Gaps
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                                                                       1. 712

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

/clone="PTB-102B07.F"

/sex="male"

/clone="lymphoblast"

/clone=lymphoblast"
                                                                                                                                                                                                                               Length 712;
                                                                                                                                                                                                                               a 34.2%; Score 455; DB 9; Length 71 Similarity 86.2%; Pred. No. 2.6e-126; 29; Conservative 0; Mismatches 76; Indels
                                                          Location/Qualifiers
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Pan troglodytes
              pKS145
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              Vector
R.Site 1
R.Site 2
LIBRARY
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Matches 529;
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AG121669/c
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Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Vokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbesegac.riken.go.jp, URL:http://hgp.gac.riken.go.jp/,
Tel:81-45-503-911, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                              1148
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Pan troglodytes DNA, clone: PTB-102B07.F, genomic survey sequence.
AG099717
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                  AGCAACGGCTACCCTCTTTGGGTTCCCTCCTTTGTATGGGAGCTCTTTTTCACTTTTT
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                                                                                                                                                                                                                                                                                                      CCATCCCTCCGGATCCACCAGGGTGTCCACTGTGCTCCTGATCCAGCAAGGCGCCCATTG
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                               ATTGCCTGAGAGCACAGGGAAGGACAAGGATTGGGATATAAACTCAGGCATTCAAGCC
                                                                                                                                                         TTCACTCTATTAAATCATGCAACTGCACTCTTTTCTGGTCCGTGTTTTTTATGGCTCAAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pan troglodytes (chimpanzee)
Pan troglodytes
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Entamoeba histolytica
Entamoeba histolytica
Enkaryota, Entamoebidae; Entamoeba.
Elkaryota, Entamoebidae; Entamoeba.
Elkaryota; Entamoebidae; Entamoeba.

Determination of clone end sequences from Entamoeba histolytica
Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library (2001)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 943
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library
Seq primmer: M13-Reverse
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                                                                                                                                                                                       GSS 27-AUG-2001
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186 TTATTGCCTGAGAGTACAGGGGAAGACAATGATCGGGATATAAACTCATGCATTGGGG 127
                                                                                                                                                                                       ACTGAGAGAGAGTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCTANCTGG
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                                                                                              84
                                                                                   CCAGCAACACCCCCTTTGGGTCCCCTCCCATTGTATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Entamoeba histolytica"
                                                                                                                                                                                                                          genomic, genomic survey sequence.
BH149565
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High quality sequence start: 40
High quality sequence stop: 567.
Location/Qualifiers
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/strain="HM1:IMSS"
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BH149565/c
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                                                                                                                                                            Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-2S Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mall:chimpbes@ger.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
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           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                   Taylor, T.D., Yada, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Pan troglodytes"
/mol type="genomic DNA"
/mol type="taxon:9598"
/db xref="taxon:9598"
/clone="PTB-130M15.F"
/est="male"
/cell type="lymphoblast"
/cell type="lymphoblast"
/cell type="pTB-thmpanzee Male BAC Library"
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                                                                 Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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AG102951 683 bp DNA linear GSS 03-NOV-2001
Pan troglodytes DNA, clone: PTB-106G16.F, genomic survey sequence.
AG102951
                                                                                                                                                                                                                                                                                                                                                                                                        GCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAAAATCTACCGTGG 372
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Totoki, Y., Watunabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359 ACCCTGGGCCAGCCTGCTAGCCCTTGCTCCGATGTAATGACATCAAAGGCACCCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGAGGAAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGGAAGCAGTTAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 TGAGGAAATCTCAACTGCACACCCTACCATGCCCCATTCAGCAGGAAGCAGGTAGAG
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                                                                                                                                                                                                                                                                 GATGCCCTGGACTCTCCCCTTCTTAGGACCTCTAGCAGCTATAATATTTTTACTCCTCTT
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                                                                                                                                                         ö
                                                                                                                     619;
                                 /sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                       Length
                                                                                                                                                         Indels
                                                                                                                     Score 435.6; DB 9;
pred. No. 2e-120;
0; Mismatches 76;
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'db_xref="taxon:9598"
              /clone="PTB-071A23.R"
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Pan troglodytes
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                                                                                                                       32.8%;
llarity 86.3%;
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                                                                                                                           Query Match
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Matches 40
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AG102951
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Totoki, Y., Watanabe, H. and Sakaki, Y.

Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Birect Submission

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@ger.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,

Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
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Pan troglodytes DNA, clone: PTB-071A23.R, genomic survey sequence.
AG076758
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 531 CAGGTAGTAAAGAGAGCTCACTAAAACGCTAATTAGGCAAAAACAGGAGGTAAAGAAATA 472
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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                                                                                                                               122 gracecederrearrerarceaecreaacarraerecreserrecaerrerer
                                       GCCAATCATCTATTGCCTGAGAGCACAGGGGAAGGACAAGGATTGGGATATAAACTCAG
                                                           TATGGCTCAAGCTGAGCTTTTGTTCGCCATCCACCACTGCTGTTTGCCACCGTCACAGAC
                                                                                                                                                                                 838 TITCACICIATITCACTCIATIAAATCAIGCAACTG--CACTCITCIGGICCGIGITITI
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BAC end sequences of Library PTB
Unpublished
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
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R.Site 1 : Sac1
R.Site 2 : Sac1.
Location/Qualifiers
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Euteleostomi;

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TGATCGGGATATAAACCCAGGCATTCGAGCCAGCAATGGCTACCCTTTTGGGTCCCTC 261
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                                                                                                                                                                                                                                                                                                                              Email: bbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchassed from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 611)
Jahos,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
Venter,J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="Lymphocytes"
/clone lib="RPC1-11"
/note="Vector: pBAce3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
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                                                                                                                                                                                                                  Unpublished (1997)
Other GSSB: RPC111-165G20.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukarryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
Email: hbe@tigr.org
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/organism="Homo sapiens"
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/db_xref="GDB:7563139"
/db_xref="taxon:9606"
/clone="RPCI-11-165G20"
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genomic survey sequence.
AQ381711
                                   AQ381711.1 GI:4352734
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                                                                      Homo sapiens (human)
Homo sapiens
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and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clonnes are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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                                                                                                                                                                                                                                                                                                                                                /sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
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al Similarity 88.6%; Pred. No. 8.1e-120;
514; Conservative 0; Mismatches 61;
                                                                                                                                                                                                                                                                        /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-106G16.F"
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                                                                                                                                                Sequencing: -21M13
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R.Site 1
R.Site 2
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Matches 514; Conserv
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El (bases 1 to 714)

RS Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.

Upublished (1998)

Other GSSs: RPCI11-64L19 TK

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RPCIII-64L19.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-64L19, genomic survey sequence.
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790 GCAACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTTCACTCTATT
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Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Direct Submission
and Chemical Research (RIKEN); Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbesoger.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-911, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
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Pan troglodytes DNA, clone: PTB-084E11.R, genomic survey sequence.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
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  492 AATTGTTCCTGCATGGCTAAGTGCCCAGGTTGGTCCTAATTGAGCTGAAGGCTAGTCACT
                                                                                      CACTGTGCTCCTGATCCAGCGAGGTACCCATTGCCACTCCCGATCAGGCTAAAGGCTTGC
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BAC end sequences of Library PTB
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db xref="taxon:9599"
/clone="PTB-084E11.R"
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
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1-7-22 Suchitro-chou, Taurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mall:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Pan troglodytes"
/mol type="genomic DNA"
/mol type="genomic DNA"
/db Aref="taxon:9598"
/clone="PTB-113D17.R"
/sex="male"
/cell type="lymphoblast"
/cell type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.9%; Score 424.4; DB 9;
llarity 82.0%; Pred. No. 5.1e-117;
Conservative 0; Mismatches 107;
                                                    Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y. BAC end sequences of Library PTB Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                   Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
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Matches 488; Conserv
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Pan troglodytes DNA, clone: PTB-113D17.R, genomic survey sequence.
AG108186
AG108186.1 GI:16728704
AG108166.1 GI:16728704
Pan troglodytes (chimpanzee)
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                                                                      / Gex="Mal:" | Cex="Male" | Cex| | Cype="Lymphocytes" | Coll type="Lymphocytes" | Coll type="Lymphocytes" | Coll type="Type" | Coll type="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCIII Human Male BAC Library"
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                                                                                                                                                                                              32.2%; Score 427.6; DB 8;
llarity 83.0%; Pred. No. 5.5e-118;
Conservative 0; Mismatches 92;
       /mol_type="genomic DNA"
|db_xref="GDB:7524474"
|db_xref="taxon:9606"
|clone="RPCI-11-64L19"
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Qy 911 GCTTTTGTTCGCCATCCACTGCTGTTTGCCACCGTCACAGACCCGCTGCTGACTTCC 970	031 ACTCCCGATCAGGCTTGCCATGTTCCTGCATGGCTAGGTTTGT	Qy 1268 CCATTITG 1275 Db 647 CATCCTIG 654 RESULT 36 CB990962 LOCUS CB990962 DEFINITION AGENCOURT 13518713 NIH MGC_148 Homo sapiens cDNA clone ACCESSION CB990962 ARAMA sequence. ACCESSION CB990962 GI:30285482	KEYWORDS EST. SOURCE Homo sapiens ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. REFERENCE I (bases 1 to 797) AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE NIH-MGC http://mgc.nci.nih.gov/. COMMENT Contact: Robert Strausberg, Ph.D. Email: Gapabs-romail.nih.gov Tissue Procurement: Dr. Stefan Hansson CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Agencourt Bioscience Corporation.	Clone distribution: Mc. Clone distribution into march condition and distribution: Mc. Clone distribution and condition and consortium/Link at: http://image.llnl.gov plate: NDAM355 row: j column: 11 High quality sequence stop: 661. High quality sequence stop: 661. Location/Qualifiers 1. 797 About type="mcMA" About type="mcMA" About type="mcMA" About type="mcMA" Alab host="mcMa" Alab host="blid Fond" Alab host = "blid Fond" Alab host="blid Fon
	χ Σ	JOURNAL Unpublished JOURNAL Unpublished Lockly, Y., Matanabe, H. and Sakaki, Y. AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. TITLE Direct Submission JOURNAL Submitted (02-400-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of	PRIMERS Sequencing: -21M13 LIBRARY Vector : pKS145 R.Site 1 : SacI R.Site 2 : SacI R.Site 2 : SacI Accation/Qualifiers 1 . 675 / organism="Pantroglodytes" / mol_type="genomic DNA" / db xref="taxon:9598" / clone="Pra-124N08.F" / sex="male" / cell type="lymphoblast" / clone="lymphoblast" / clone="lib="TB" Chimpanzee Male BAC Library"	Query Match 31.94; Score 423.8; DB 9; Length 675; Best Local Similarity 83.94; Pred. No. 7.7e-117; Pred. S. 7.7e-117; Agaba 2; Qy 671 GAGCTCACTAAATGCGAAAACAAGGAGTAAAGCAATGCCAATCATGT 730 St. Indels 20; Gaps 2; Qy 673 GAGCTCACTAAAATGGCAAACAAGGATAGAAAAAAAAAA

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/use transmission and the contract of the cont
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AGENCOURT 13642588 NIH_MGC_148 Homo sapiens cDNA clone
IMAGES33336351 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 803;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 422.2; DB 6;
Pred. No. 2.5e-116;
0; Mismatches 59;
ity sequence stop: 552.
Location/Qualifiers
                                                     1. .803
/organism="Homo
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CB990802.1 GI:30285322
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ilarity 88.5%;
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Email: Cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Stefan Hansson

CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
thtp://image.llnl.gov

Plate: NDAM362 row: a column: 12
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1 (bases 1 to 803)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                             91
     Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 GATCCTGCAGGGGTGTCCGCTGTGCTCTGATCCAGCGAGGCGCCCATTGCCGCTCCCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     392 TATAACACTTACCACTGGCCCAAGATTCCATTCCTTGGAATCCGTGAGGCCAAGAACTC
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                                                                                                                                                                                                                                                                                               34 CCCCCTTTGGGTCCCTTCCTTTGTATGGGAG--CTGTTTTCATGCTATTTCACTCTATT
                                                                                                                                                                                                                                                                                                                                                                   860 AAATCATGCAACTGCACTCTTCTGGTCCGTGTTTTTTATGGCTCAAGCTGAGCTTTTTTGTT
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AGENCOURT 13623067 NIH MGC_148 Homo sapiens cDNA clone
IMAGE:30337259 5', mRNA sequence.
                                                                                                                                           Length 797;
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                                                                                                                                                                                                    Indels
                                                                                                                                                Score 422.2; DB 6;
Pred. No. 2.5e-116;
); Mismatches 59;
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CB992422.1 GI:30286942
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Homo sapiens
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Matches 469; Conservative
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980 GATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGCGAGGTACCCATTGCCACTCCCGAT 1039
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452 CAGGICAGAGAAIACGAGGCIIGCCACCAICTIGGAAGCGGCCIGCTACCAICTIGGAAG 511
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                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with he and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM348 row: p column: 01
High quality sequence stop: 611.
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AGENCOURT 13617032 NIH MGC_148 Homo sapiens cDNA clone
IMAGE:30332232 5′, mRNĀ sequence.
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                                                          512 TGGTTCACCACCATCTTGGGAGCTCTGTGAGCAAGGACCCCCGGGTAACA
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Pred. No. 2.5e-116;
0; Mismatches 59;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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al Similarity 88.5%;
469; Conservative
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   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                     Email: cgapbe-remail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with
and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequenocing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   860 AAATCATGCAACTGCACTCTTCTGGTCCGTGTTTTTATGGCTCAAGCTGAGCTTT
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Pred. No. 2.5e-116;
0; Mismatches 59;
                                                                                                                                                                                                                                                                                                          Plate: NDAM359 row: k column: 16
High quality sequence stop: 585.
Location/Qualifiers
                                                                                                                        Contact: Robert Strausberg, Ph.D.
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llarity 88.5%;
Conservative 0
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/clone="InWAGE:30339155"
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/clone_lib="NIH MGC_148"
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all.xhoi; Site_2: Bandl; Library is oligo-dT primed and directionally cloned using primer
5. TTTTTTTTTTTTTTTTVN-3; size-selected for average insert
size_3: Ab and normalized to ROT 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIMH/NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Concact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
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CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information clone found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM366 row: p column: 12
High quality sequence stop: 708.
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                                                            CAGGCTAAAAGGCTTGCCATGTTCCTGCATGGCTAAGTGCCTGGGTTTGTCCTAATAGAA 1099
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NIH-MGC http://wgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
CAGGTCAGAGAANGTGAGGCTTGCCACCATTTGGGAAGTGGCCCACTGCCATTTTGGTAG
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AGENCOURT 13633532 NIH MGC 148 Homo sapiens cDNA clone IMAGE:30339155 5', mRNA sequence.
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CB994833.1 GI:30289353
EST.
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Homo sapiens
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KEYWORDS
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                                    Indels
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9
Score 422.2; DB 6;
Pred. No. 2.5e-116;
0; Mismatches 59;
   31.8%;
 Query Match
Best Local Similarity 88.5
Matches 469; Conservative
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Search completed: February 21, 2005, 14:51:22 Job time : 4143.82 secs